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Sequence Strd Orig ZSCORE ESCORE Len 1 Documentation /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF58602 + 946.00 1 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:AAS64474 + 650.50 1 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:AAN91477 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:AAA011642 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:AAA32150 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:AAA33150 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1901.DAT:AAA158380 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAA158380 + 649.50 11 /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT
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Query length:
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Database sequences: 1736436
Database length: 858457221
Search time (sec): 175.470000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame+_p2n.model -DEV=x1h
-Q-/cgn2_1/USPF0_spco1/US10031904/runat_09102002_084257_23681/app_query.fasta_1.232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA09026 + /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAI60166 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-031-904-8
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:AAX70048
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:AAX91044
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                          The present sequence encodes a human RECAP (receptors and associated CC proteins) polypeptide. RECAP polypucleotides and polypeptides are useful in the diagnosis, treatment and prevention of neurological disorders such as stroke, Alzheimer's disease, Pick's disease, Huntington's CC disease, dementia, Parkinson's disease, Downs's syndrome, amyotrophic lateral sclerosis, multiple sclerosis, bacterial and viral meningitis, CC disease, Discoural and viral meningitis, CC disease, Immunological disorders, including autoimmune/inflammatory CC disorders such as AIDS, DiGeorge's syndrome, severe combined CC disorders such as AIDS, DiGeorge's syndrome, severe combined CC disease, Addison's disease (SCID), Chediak-Higashi syndrome, Cushing's CC disease, Addison's disease, autoimmune thyroiditis, Crohn's diseases, CC disease, Thyroiditis, Sjogren's syndrome, Yenre's diseases, CC disease, Thyroiditis, Sjogren's syndrome, Werner's syndrome, viral, Bacterial, fungal, parasitic, protozoal, and helminthic infections; and cell proliferation disorders such as arteriosclerosis, atherosclerosis, cirrhosis, hepatitis and cancer.
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07-OCT-1999;
12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 120; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Novel receptors and associated proteins for diagnosis and treatment of neurological disorders, immunological disorders including autoimmune/inflammatory disorders and cell proliferative disorders such as cancer
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Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2000;
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DB; AAB68878.
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99US-0158578.
99US-0165192.
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Patterson C, Lal P;
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alignment_scores:

Quality:

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Length:

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Sequence 627 BP;

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAS64474
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                                                                                                                                                                                                                                                                                                                                       _documentation_block:
AAS64474 standard; cDNA; 7821 BP.
                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #278.
30-MAR-2001; 2001WO-US08631.
                                          11-OCT-2001.
                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                          13-FEB-2002 (first entry)
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                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eHisSerAsnPheSerLeuGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGTTTGTGACAGTGAGTTGAAATATGCATTCCTATTTCTTTTACCGAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCACATGCATCATCTCAGGCAACACTGTCATTTGGGATAATAAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTCGT
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The invention relates to isolated polynucleotide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences and for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO of the polypeptide in the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of the polypeptide and polypeptide in electronic format directly from WIPO of 
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Sequence 7821 BP; 1986 A; 1904 C; 1883 G; 2046 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 278; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                    at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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647 CCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAG
                                                                                                                                                                                       597 AATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTT
                                                                                                                                                                                                                                                                                   547 CGTGGTGCTGCCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                               497 CAGCCGGCCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGT 546
                                                                                                                          56 ProIleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyAr 72
                                                                                                                                                                                                                 39 luTrpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhe 55
                                                                                                                                                                                                                                                                                                                            23 aLeuValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProG 39
                                                                                                                                                                                                                                                                                                                                                                                                                        9 ArgProPheProSerArgArgPhe.....ProGlyLeuLeuLeuAlaAl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650.50
4.854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 7821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.208
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seq_documentation_block:
ID AAN91477 standard; DNA; 6951 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:AAN91477
                                                        This is full-length CR1 protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertes activity. They are useful in diagnosing and treating immune disorders, and preventing are useful in diagnosing and treating immune disorders, and preventing are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement; cofactor.
                                                                                                                                                                        Claim 1; fig. 1; 191pp; English.
                                                                                                                                                                                                                 New nucleic acid sequences encoding new CRI protein - and its fragment, for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc
                                                                                                                                                                                                                                                                                                         WPI; 1989-309498/42.
P-PSDB; AAP92219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR1 protein DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN91477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 leSerGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154 [|||||||||:::|||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 TTGTACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 rCysProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 MetAlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TCEL-) T CELL SCIENCES INC.
(UVJO ) THE JOHNS HOPKINS UNIVERSITY.
(BRIG ) THE BRIGHAM AND WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         897 TCTCAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 797 ATGGTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTC 846
Sequence 6951 BP; 1802 A; 1680 C; 1660 G; 1809 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1990 (first entry)
                                           perfusion injury.
                                                                                                                                                                                                                                                                                                                                                                        Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88US-0176532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-US01358.
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28..6147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
1..6951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note="CR1 protein"
28..1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 28..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="CRI protein"
                                                                                                                                                                                                                                                                                                                                                                        Wong W, Carson G,
                                                                                                                                                                                                                                                                                                                                                                        Concino MF,
                                                                                                                                                                                                                                                                                                                                                                        Makrides SC;
  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/Na1991.DAT:AAQ11642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAN91477 from: 1 to: 6951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-031-904-8 x AAN91477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 CAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 erGlyAsnThrVallleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9105047-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 GGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 GGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCC 219
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                            Entire human complement type 1 receptor coding region
                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ11642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ11642 standard; DNA; 6951 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
                                                                                mat_peptide
                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                          complement system; C3b/C4b receptor; CR1; allergic reaction; immune response; clone lambda T109.1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                /*tag= a
/note= "putative"
148..6144
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4.883
89.865
                                                                                                                                                                     Location/Qualifiers
                                           /product= C3b/C4b receptor
                                                               /*tag=
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Gaps: 2
Percent Identity: 81.757
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AC XXX XXX AC XX

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SSSSSSSSXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAQ11642 from: 1 to: 6951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-031-904-8 x AAQ11642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a composite of sequences isolated as lambda clones H10.3, T109.1, H3.1 and H7.1. The clones were present in the specifically primed lambda 9tl1 cDNA library (Lambda HH) which was prepared with cDNA synthesised from poly(A)+ RNA from DMSO induced H1.-60 cells. The library was screened using probes CR1-1, CR-2 and CR1-4 (see Mong, WW et al., 1985, Proc. Nat. Acad. Sci. USA. 82:7711) and probe CR1-18 (corresponding to nucleotides 101-352 of this sequence). There are four direct, long homologous repeats of 450bp, each comprising 7 short consensus repeats. Nucleotides 28-1533 are also claimed separately.
Claim 1; Fig 1; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial infarct, damage due to inflammmation and in treatment of thrombosis
                                                                          270 GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACA 319
                                                                                                                                                   220 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC
                                                                                                                                                                                        57
                                                                                                                                                                                                                         170 GGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCC
                                                                                                                                                                                                                                                                                                  120 GGTGCTGCGTGCCGGTGGCCTGGGGTCAATGCCAATGCCCCAGAAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6951 BP; 1802 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR11810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TCEL-) T CELL SCI INC.
(UYJO ) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1989;
26-SEP-1990;
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                                                                                                                                                                                                                                                                                                                         25-SEP-1990;
                                                                                                             73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
                                                                                                                                                                                                                                                          40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
                                                                                                                                                                                                                                                                                                                                                                          70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                              10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe 24
                                                                                                                                                                                      ileGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgPr 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1991-132854/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marsh HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-0412745
90US-0912349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              649.50
4.883
89.865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 81.757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1681 C; 1659 G; 1809 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carson GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoh M,
                                                                                                                                                   269
                                                                                                                                                                                                                           219
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAZ38150
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06-DEC-1974;
24-FEB-1993;
01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ38150 standard; DNA; 6951 BP
                             -length human CR1 as expressed on erythrocytes. The CR1 function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CR1 protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CR1 protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CR1 proteins, analogues, derivatives, and anti-CR1 antibodies are used in assays, and diagnostics. The present sequence represents a DNA encoding the human CR1 protein.
                                                                                                                                                                                                                                     The invention relates to a human C3B/C4B receptor (CR1) protein. The CR1 protein on fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full-length human CR1 as expressed on erythrocytes. The CR1 function in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Concino MF, wony ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3B/C4B receptor; CRI protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                  A human C3B/C4B receptor (CR1) protein having antiinflammatory and cardiant activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-633357/54.
P-PSDB; AAY55751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 CAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 erGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS
                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1A-P; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human C3b/C4b receptor (CR1) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AlaHisValIIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
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74US-0350238.
93US-0026134.
88US-0176532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makrides SC, Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IP SH;
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Sequence 6951 BP; 1802 A; 1680 C; 1661 G; 1808 T; 0 other;

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alignment_scores:
seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAZ38150 from: 1 to: 6951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-031-904-8 x AAZ38150
                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS;
Alkheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 erGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 GGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GGTGCTGCTTGCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAGAAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 CAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC 269
                   26-DEC-2000; 2000WO-US34263.
                                                                                                                     WO200153312-A1
                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 583.
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI58380 standard; cDNA; 7313 BP.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                               leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 oPheSexIleIleCysLeuLysAsnSerValTrpThrSexAlaLysAspL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysCysLysArgLysSerCysArgAsnProProAspProValAsnGlyMet 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                        thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649.50
4.883
89.865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 81.757
                                                                                                                                                                                                                                        drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
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alignment_block:
US-10-031-904-8 x AAI58380
                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                   Align seg 1/1 to: AAI58380 from: 1 to: 7313
                                                                                                                                                                                                                 Percent Similarity:
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activiny, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 583; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - {\sf}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                   Sequence 7313 BP; 1903 A; 1770 C; 1733 G; 1907 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                        specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAM39224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
                                     70 CCGGCGCCCGGTCTCCCCCTTCTGCTGCGGATCCCTGCTGGCGGTTGT 119
                                                                           10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-442253/47.
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                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asundi V, Ch
Wehrman T, X
, Goodrich R,
                                                                                                                                                                                                                   649.50
4.883
89.865
                                                                                                                                                                                                          Length: 148
Gaps: 2
Percent Identity: 81.757
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Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, 1
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
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220 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC 269

57 IleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgPr 73

170 GGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCC 219

40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56

120 GGTGCTGCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAGAAT 169

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABA09026
Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopolesis regulation; tissue growth; immunomodulator; activin; inhibit; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiaflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 707-709; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB11782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CR1 protein homologue-encoding cDNA, SEQ ID NO:802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
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us-10-031-904-8 x ABA09026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: ABA09026 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haematopoiesis requiatory activity; tissue growth activity; conditions requiatory activity; tissue growth activity; conditions, activity; activities; haemastatic, thrombotic or chemokinetic activities; haemastatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders, chronic inflammatory conditions (e.g., asthma or arthritis), coronary heart disease, and abnormal conditions, and abnormal conditions include activities, bone disorders (e.g., osteoporosis), and abnormal constitution of uncleic acids encoding them may be used to promote wound conditions to municondulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to promote cell growth. For example, such polypeptides may be used to complete stem cells in culture to give rise to neuroepithelial cells can be used to autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used to the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 GGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GGTGCTGCTTGCGCTGCCGGTGGCCTGGGGTCAATGCCAATGCCCCAGAAT 169
106 tAlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerC 123
                                                                 320 AGGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCAT 369
                                                                                                                                                                                             270 CGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGAC 319
                                                                                                                                                                                                                                                                                                                             220 CATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7028 BP; 1819 A; 1704 C; 1681 G; 1824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                  73 roPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAsp
                                                                                                                                                                                                                                                                                                                                                              56 OIleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                    90 LysCysLysArgLysSerCysArgAsnProProAspProValAsnGlyMe 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 rp.LeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe
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4.786
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420 GTACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATC 469

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seq_documentation_block:
ID AAI60166 standard;
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                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ActivinyInhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, days creening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, and the contractivity and concerdiagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 4155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 TCAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4155; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM41010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI60166 standard; cDNA; 7028 BP
                                                  specification.
                                                                                                                             assays for receptor activity, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 -SEP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                  .N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGlyAsnThrVallleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QA,
                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-06633036.
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2000US-0552317.
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Wehrman T, X
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                and inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J;
                                                                                                                                leukaemias and
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170
                       11-SEP-1998
                                                                             WO9839433-A1
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Sequence 7028 BP; 1819 A; 1704 C; 1681 G; 1824 T; 0 other;

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV53262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAI60166 from: 1 to: 7028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-031-904-8 x AAI60166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                          Complement receptor type-1; CR1; CM7; complement; inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 TCAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 SerGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 GTACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ysProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIle 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 GGTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 CATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGAC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GGTGCTGCCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAGAAT 169
                                                                                                                                                                                                                                                                                                                                                Complement receptor type 1-like sequence CM7 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV53262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV53262 standard; DNA; 591 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 tAlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AGGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 CGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGAC 319
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 LysCysLysArgLysSerCysArgAsnProProAspProValAsnGlyMe 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 roPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAsp 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 oIleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 rp.LeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ProPheProSerArgArgPhe.....ProGlyLeuLeuLeuAlaAlaLe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGGAGGATCCCTGCTGGCGGGTTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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89.262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-031-904-8 x AAV53262
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                                                                                                                                                                                                                                                                                                                    104
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100 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 591 BP; 132 A; 159 C; 148 G; 152 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-506358/43.
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                                                                                                                                                                                                                                                                                                                                                           67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inappropriate complement activation
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                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 TGATGAATTTGAGTTCCCGATCGGTACCTACCTGAACTACGAATGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CAGTGCAACGCTCCGGAATGGCTGCCGTTCGCGCGCCCCGACCAACCTGAC 53
                                                                                                                                    TGGACTGGTGCTAAGGACCGTTGCCGACGTAAATCTTGTCGTAATCCGCC 203
                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mossakowska DEI,
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5.336
98.347
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seq_documentation_block:
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        This DNA sequence encodes CM1 (see AAW79237), a protein that consists CC of the short consensus repeats (SCR) 1 and 2 from complement CC receptor type 1 (CR1) fused to an SCR3 (see AAW79242) in which 5 amino CC acids were altered to those found in the SCR3 of the CR1-like pseudogene (Cripse) putative product. CM1 DNA was constructed by CC site-directed mutagenesis (see AAW53263) of plasmid pbBJD13-5. which codes for SCR1-3 of CR1. pBrocSCR1-30M1 carrying CM1 DNA was used CC totransform Escherichia coll BL2(DE3), and CM1 was purified from CC solubilised inclusion bodies. The invention provides DNA sequences (see AAW53262 and AAV53269-79) encoding novel soluble engineered CR1 collubilised inclusion bodies. The invention provides DNA sequences (see AAW53252 and AAV53269-79) encoding novel soluble engineered CR1 collubilised inclusions at the second complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or construction, such as neurological disorders (e.g. multiple sclerosis activation, such as neurological disorders (e.g. multiple sclerosis complement activation (e.g. venouraft rejection). Inflammation or complement activation (e.g. venouraft rejection).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement receptor type-1; CR1; CM1; complement; inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 erGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 ACCGATTTGTGAC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AGCGCTACATGCATCATCTGGGGATACTGTCATTTGGGATAATGAAAC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 44; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 rProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 CCCAAATTAAATATTCTTGTACTAAAGGTTACCGTCTGATTGGTTCCTCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AGATCCGGTTAACGGCATGGTGCATGTGATCAAAGGCATCCAGTTCGGTT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9839433-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inappropriate complement activation
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complement activation (e.g. xenograft rejection), inflammatory

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     seq_documentation_block:
ID AAV53270 standard; DNA; 591 BP.
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                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV53270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAV53269 from: 1 to: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ignment_block:
US-10-031-904-8 x AAV53269
                                                                         Complement receptor type-1; CR1; CM2; complement, inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmne disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), post-ischaemic reperfusion conditions, infection or sepsis, immune complex disorders and autoimmune diseases (e.g. rheumatoid arthritis, proliferative nephritis and myasthenia gravis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                       134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 erGlnlleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
                                                                                                                                                                                      Complement receptor type 1-like sequence CM2 DNA.
                                                                                                                                                                                                                   18-JAN-1999 (first entry)
                                                                                                                                                                                                                                                  AAV53270;
                                                                                                                                                                                                                                                                                                                                                            354 ACCGATTTGTGAC 366
                                                                                                                                                                                                                                                                                                                                                                                          150 rProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                          304 AGCGCTACATGCATCTCTGGTGATACTGTCATTTGGGATAATGAAAC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 CCCAAATTAAATATTCTTGTACTAAAGGTTACCGTCTGATTGGTTCCTCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AGATCCGGTTAACGGCATGGTGCATGTGATCAAAGGCATCCAGTTCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 TGGACTGGTGCTAAGGACCGTTGCCGACGTAATCTTGTCGTAATCCGCC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 CGGGTTATAGCGGCCGGCCCGTTTTCTATCATCTGCCTGAAAAACTCTGTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 591 BP; 127 A; 159 C; 151 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive disorders.
   WO9839433~A1
                               Synthetic.
                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 TGATGAATTTGAGTTCCCGATCGGTACCTACCTGAACTACGAATGCCGCC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
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5.336
98.347
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Gaps: 0
Percent Identity: 90.909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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100 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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co fithe short consensus repeats (SCR) 1 and 2 from complement creceptor type 1 (CRI) fused to an SCR3 (see AAW79243) in which 4 amino codes were altered to those found in the SCR3 of the CRI-like pseudogene (Cripse) putative product. CMZ DNA was constructed by steredirected mutagenesis (see AAW53264) of plasmid pDB1013-5, which Cc codes for SCR1-3 of CR1. pBrocSCR1-3CM2 carrying CM2 DNA was used ct otransform Escherichia coli BLA1(DB3), and CM2 was putified from CC solubilised inclusion bodies. The invention provides DNA sequences (see AAW53262-79) encoding novel soluble engineered CR1 CC polypeptides (see AAW53269-79) encoding novel soluble engineered CR1 CC inhibitors with functional complement inhibitory, including cantivation, such as neurological disorders (e.g. multiple sclerosis and latvation, such as neurological disorders (e.g. multiple sclerosis complement activation, such as neurological disorders (e.g. multiple sclerosis and parkinson's disease), disorders of inappropriate or undesirable CC complement activation (e.g. xenograft rejection), inflammatory clischaemic reperfusion conditions, infection or sepsis, immune complex disorders and autolumnune diseases (e.g. rheumatoid cr reproductive disorders and autolumnune diseases (e.g. rheumatoid cr reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation inappropriate complement activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 45; 67pp; English.
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Sequence 591 BP; 134 A; 158 C; 146 G; 153 T; 0 other;

alignment_block: US-10-031-904-8 x AAV53270 635.00 5.336 98.347 Percent Identity: 90.909

Align seg 1/1 to: AAV53270 from: 1 to: 591

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seq_documentation_block:
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            This DNA sequence encodes CM2 (see AAW79239), a protein that consists of the short consensus repeats (SCR) and 2 from complement receptor type 1 (CR1) fused to an SCR3 (see AAW79244) in which 1 amino acid was altered to that found in the SCR3 of the CR1-like pseudogene (Cr1pse) putative product. CM3 DNA was constructed by seudogene (Cr1pse) putative product and the SCR3 of plasmid pDB1013-5, which codes for SCR1-3 of CR1. pBrocSCR1-3CM3 carrying CM3 DNA was used to transform Escherichia coli BLZ1(DE3), and CM3 was putified from solubilised inclusion bodies. The invention provides DNA sequences (see AAW33262 and AAW33269-79) encoding novel soluble engineered CR1 (see AAW33262 and AAW33269-79) encoding novel soluble engineered CR1 inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement and various and beautions, such as neurological disorders (e.g. unlipse solerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement receptor type-1; CR1; CM3; complement; inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohm's disease; astima; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation inappropriate complement activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 46; 67pp; English.
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Parkinson's disease), disorders of inappropriate or undesirable
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DB; AAW79239.
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US-10-031-904-8 x AAV53271
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ID AAV53272 standard; DNA; 591 BP
   seq_name: /SIDS1/gcgdata/geneseq/geneseqn~emb1/NA1998.DAT:AAV53272
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                                                                                                 Complement receptor type-1; CRI; CMS; complement; inhibitor; anti-haemolytic; multiple scierosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
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                            Synthetic.
                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                           Complement receptor type 1-like sequence CM5 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGTTATAGCGGCCGCCCGTTTTCTATCATCTGCCTGAAAAACTCTGTC
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Ratio:
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alignment_block:
US-10-031-904-8 x AAV53272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudogene (Cripse) putative product. CM5 DNA was constructed by call pseudogene (Cripse) putative product. CM5 DNA was constructed by codes for SCR1. 3 of CR1. pseroSCR1-30M5 carrying CM5 DNA was used to transform Escherichia coli BL21(DE3), and CM5 was purified from columnia serior section of the serior section of the serior section of the serior section of the section of the section provides DNA sequences (see AAV53262 and AAV53269-79) encoding novel soluble engineered CR1 polypeptides (see AAW532647) such as CM5 that act as complement inhibitory, including novel soluble engineered cR1 polypeptides (see AAW532647) such as cM5 that act as complement complement inhibitory, including not inhibitory, including the section of the sec
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                                                                                                                                       104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW79240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADPR-) ADPROTECH PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive disorders.
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                                                                                                                                                                          67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                                                                                                                                                                                                                                          54 TGATGAATTTGAGTTCCCGATCGGTACCTACCTGAACTACGAATGCCGCC 10:
                                                                                                                                                                                                                                                                                                                                            50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
                                                                                                                                                                                                                                                                                                                                                                                                              4 CAGTGCAACGCTCCGGAATGGCTGCCGTTCGCGCGCCCGACCAACCTGAC 53
TGGACTGGTGCTAAGGACCGTTGCCGACGTAAATCTTGTCGTAATCCGCC 203
                                  TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
                                                                                                                                   CGGGTTATAGCGGCCGCCCGTTTTCTATCATCTGCCTGAAAAACTCTGTC 153
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seq_documentation_block:
ID AAV53273 standard; DNA; 591 BP
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This DNA sequence encodes CM6 (see AAW79241), a protein that consists of the short consensus repeats (SCR) 1 and 2 from complement receptor type 1 (CR1) fused to an SCR3 (see AAW79246) in which 6 amino acids were altered to those found in the SCR3 of the CR1-like pseudogene (Cr1pse) putative product. CM6 DNA was constructed by stie-directed mutagenesis (see AAW32363 and AAW32365) of pDB1013-5, which codes for SCR1-3 of CR1. pBrocSCR1-3CM6 carrying CM6 DNA was used to transform Escherichia coll BL21(DE3), and CM6 was purified from Sclubilised inclusion bodies. The invention provides DNA sequences (see AAW53262 and AAW53269-79) encoding novel soluble engineered CR1 collypoptides (see AAW53269-74) such as CM6 that act as complement inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement consociated with inflammation or inappropriate complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement receptor type-1; CR1; CM6; complement; inhibitor; anti-lamentyltic; multiple sclerosis; parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthitis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation inappropriate complement activation
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                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 48; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97GB-0004519
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/wa1993.DaT:AAQ41867
                                                                                                                                                                                                                                                                                                                                                                                                                     9q_documentation_block:
                              (3b/C4b receptor; CR1; erythrocyte; monocyte; macrophage; granulocyte; tC3b; T cell; splenic follicular dendritic cell; soluble; complement; glomerular podcoyte; B cell; C3b; C4b; inactivated C3b; phasgocytots1s; plasma; ligand binding activity; immune complex; activator; allotype; endocytosis; lymphocyte; classical; alternative; pathway; cofactor; P; C3/C5 convertase; liver; cleavage; factor I; regulation; glycoprotein; S; A; B; glycosylation; duplication; repetitive intervening sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 ACCGATTTGTGAC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                      endoglycosidase F; ss.
                                                                                                                                                                                                                                          CR1 coding region.
                                                                                                                                                                                                                                                                                            14-SEP-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), post-ischaemic reperfusion conditions, infection or sepsis, immune complex disorders and autoimmune diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                          AAQ41867 standard; DNA; 6951 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTGCAACGCTCCGGAATGGCTGCCGTTCGCGCGCCCGACCAACCTGAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGCTACATGCATCATCTCTGGGGATACTGTCATTTGGGATAATGAAAC 353
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CC molecular weight as membrane-associated CRI. SCRI binds C3b and C4b CRI that have covalently attached to immune complexes and other complement CC activators. The consequences of these interactions depends on the CC type of bearing the receptor. Erythrocyte CRI binds immune complexes if or transport to the liver. CRI on neutrophils and monocytes internalises bound complexes, either by adsorptive endocytosis. CC or by phagocytotsis. The function of CRI on B lymphocytes is less CC well defined. CRI can inhibit the classical and alternative pathway CC C3/C5 convertases and act as a cofactor for the cleavage of C3b and C4b by factor I, therefore CRI has a complement regulatory function CRI as well as acting as a receptor. CRI is a glycoprotein composed of CC a single polypeptide chain. Four allotypic forms of CRI have been CC identified, differing by increments of approx. 40-50 kD. The two most CC may molecular weights of 250 and 290 kD respectively. The two rarer CC forms have molecular weights of 250 and 290 kD. These differences CC glycosylation state because they are not abolished by treatment of CRI prified receptor portein with endoglycosidase F. The CRI gene has CC been shown to have repetitive intervening sequences which may have conducted in the formation of the larger allotypes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the entire coding region for the C3b/C4b receptor (CR1). CR1 is present on erythrocytes, monocytes/macro-phages, granulocytes, B cells, some T cells, splenic follicular dendritic cells and glomerular podocytes. CR1 specifically binds C3b, C4b and inactivated C3b (1C3b). A soluble form of the receptor is found in plasma which has ligand binding activity and the same molecular weight as membrane-associated CR1. CR1 binds C3b and C4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity - used to prevent repersusion sujuty, simple reaction and neutrophil mediated tissue damage and reduce
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Sequence 6951 BP; 1799 A; 1692 C; 1648 G; 1807 T; 5 other;

alignment_scores:
 Quality: alignment_block: US-10-031-904-8 x AAQ41867 Quality: 634.50 Ratio: 4.844 Percent Similarity: 89.726 Align seg 1/1 to: AAQ41867 from: 1 to: 6951 370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419 107 AlaHisVallleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123 320 GGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATG 369 10 ProPheProSerArgArgPhe......ProGlyLeuLeuAlaAlaLe 24 70 CCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGT 119 Length: 146 Gaps: 2 Percent Identity: 81.507

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gb_pat:AX078362
gb_pr:HSCR1
.gb_pr:CHPCR1X
gb_pr:CHPCR1WT
gb_pr:HSCR1RS
gb_sts:G28591
gb_pat:A86593
gb_pat:A86601
                                                                                                                        gb_ro:GPICRRP
gb_ro:MUSCR2AB
gb_pr:HUMCR1L2
gb_pr:HUMCR1SF02
gb_pr:HUMCR102
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gb_htg:AL160003
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Database length: 1873333701
Search time (sec): 1840.610000
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Database: GenEmbl:*
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1.6e-57
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i X14362 Human CRI mRNA for C3b,

i X14362 Human CRI mRNA for C3b,

i 28591 human STS SHGC-35372,

i A86693 Sequence 2 from Patent W

A86601 Sequence 10 from Patent

i A86601 Sequence 12 from Patent

i A86605 Sequence 14 from Patent

i A86605 Sequence 16 from Patent

i A86607 Sequence 16 from Patent

i A86607 Sequence 18 from Patent

i A86607 Sequence 18 from Patent

i A86607 Sequence 3 from Patent

i A86607 Sequence 3 from Patent

i AR02919 Sequence 3 grom Patent

i AR02919 Sequence 3 grom Patent

i AR02919 Papio cynocephalus complet

i L77977 Papio cynocephalus complete

i L77978 Papio cynocephalus complete
M31231 Human complement receptor L17399 Human complement receptor M31239 Human complement receptor M31239 Human complement receptor M3446 Mus musculus complement M8146560 Sequence 1 from pater 1 W87920 Cercopithecus aethiops m 1 D63811 African green monkey mF 1 AF025483 Saimiri sciureus CD46
                                                                                                                                                                                                                                                 | M23529 Mus musculus complement
| M16179 Mouse X/Y protein mRNA,
09 | ALL60003 Homo sapiens chromc
| M77760 Guinea pig CRRP protein
| M36470 Mouse complement recept
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gb_pat:AR112402
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AUTHORS
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ORGANISM
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Ratio: 5.437
Percent Similarity: 100.000
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                                                                                                       GATCCTGTGAATGGCATGGCACATGTGATCAAAGACATCCAGTTCGGATC
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seq_name: gb_pat:AX078362
                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                             1 (bases 1 to 627)
Au-Young, J., Bandman, O., Tang, Y.T., Yue, H., Azimzai, Y., Burford, N., Baughn, M.R., Lu, D.A., Hillman, J.L., Patterson, C. and Lal, P. Receptors and associated proteins Receptors and associated proteins Patent: WO 0107612-A 30 01-FEB-2001; Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  AX078362 627 bp
Sequence 30 from Patent W00107612.
                                                                                                                                                                                                                                                                                                                                                AX078362.1 GI:13158031
/organism="Homo sapiens"
/db xref="taxon:9606"
/note="Incyte ID No: 103561CB1"
/note="173 c 128 g 184 t
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903
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17/0308 Sequence 11 from pate
DB4105 Human CD46 mRNA, com
1 AR112400 Sequence 1 from pa
1 AR112402 Sequence 3 from pa
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Percent Identity: 100.000

Align seg 1/1 to: AX078362 from: 1 . 6

1 MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr oGlyLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34 ATGGCGCCTCCCGTCCGTCCGAGCGTCCCTTTCCTTCCCGGCGCTTTCC 186

236 50

GATGACTTTGAGTTTCCCATTGGGACATATCTGAACTATGAATGCCGCCC AspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgPr 67

rpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPro 100 oGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerValT TGGTTATTCCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTCT 336

84

AspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlySe 117

rGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerS 134

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REFERENCE
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 CCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTCGT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erAlaThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eHisSerAsnPheSerLeuGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCCACATGCATCATCTCAGGCAACACTGTCATTTGGGATAATAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATTCTAATTTTTCTCTGGAA 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGTTTGTGACAGTGAGTTGAAATATGCATTCCTATTTCTTTTACCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Fearon,D.T.

Identification of distinct C3b and C4b recognition sites in the human C3b/C4b receptor (CR1, CD35) by deletion mutagenesis J. Exp. Med. 168 (5), 1699-1717 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klickstein, L.B., Bartow, T.J., Miletic, V., Rabson, L.D., Smith, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-OCT-1988) Klickstein L.B., Room 617 Hunterian Bldg., 725 N. Wolfe St., Baltimore, MD 21205 2 (bases 1 to 1521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3b/C4b complement component receptor; C3b/C4b receptor; CD35 antigen; complement receptor; glycoprotein; membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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28. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1532-6951 are already published see x05309 Data kindly (16/5/89) by Klickstein L. Location/Qualifiers
                                                                             GDF1STNRENFHYGSVVTYRCNPGSGGRKVFELVGEPS1YCTSNDDQVGIWSGPAPQC
IIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPEL
PSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSP
                                                                                                                                                             RVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRG
AASMCTPQGDWSPAAPTCEVXSCDDFWGQLLNGRVLFPVNLQLGAKVDFVCDSGFQL
KGSASYCVLAGMESLWNSSVPVCEQIFCPSPDYLPNGRHTGKPLEVFPFGKAVNYTC
DFHEDRGTSFDLLGESTIRCTSDPQGNCVWSSPAPRCGILGHCQAPDHFLFAKLKTQT
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VTDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPFTIAN
                                                                                                                                                                                                                                                                                                                                 APEWLPFARPTNLTDEFEFFIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKDRCRRK
SCRWPDDFVNGMYHYIKGIQFGSQIKYSCTKGYRLIGSSSARCIISGDTYUWDNETFFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CR1 precursor protein"
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Align seg 1/1 to: HSCR1
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123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS 140
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                                                                                                                                    107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                      73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419
                                                                                                                                                                                                                                                                                                                                                          GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro
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1501. 2850
1501. 2850
Inote="long homologous repeat B coding sequence 2851. 4209
Inote="long homologous repeat C coding sequence"
4210. 5565
Inote="long homologous repeat D coding sequence"
1661 g 1808 t
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4.883
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ILVSDNRSLESLNEVVEERCQPGFVMKGPRVECQALNKWEEELESGSRVCQPPPEIL
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STTCLYGGNNVTWDKKAPICEIISCEPPTISNGDFYSNNKTSPHNGTVAFGNRSFS
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SVPAACPHPPKIQNGHYIGGHYSLYLPGMTISYTCDPGYLLVGKGFIFCTDQGIWSQL
DHYCKEVNCSFPLFMNGISKELEMKKYYHYGDYYTLKCEDGYTLEGSPWSQCQADDRW
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151. .1500
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FSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKSCDDFLGQLPHGRVLLP
LNLQLGARVSFVCDEGFFLKGRSASHCYLAGWKALWASSVPYCEQIFCPNPPAILAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYS
CTTGHRLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQGGSSVHPRTLQTNEENSRVLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPPLAKCTSRAHDALIVGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLH
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Percent Identity: 81.757
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SOURCE
ORGANISM
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LOCUS CHPCR1x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                           alignment_block:
US-10-031-904-8 x CHPCR1X
                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                  Align seg 1/1 to: CHPCR1X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
erGlyAsnThrValI1eTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.24921.1 GI:557726
alternative splicing product;
Pan troglodytes cDNA to mRNA.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes alternatively L24921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birmingham, D.J., Shen, X.P., Hourcade, D., Nickells, M.W. and Atkinson, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primary sequence of an alternatively spliced form of CR1. Candidate for the 75,000~\text{M}(\text{r}) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                         521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Translation="SLLAVVVLLALPVAMGQCNAPEMLPFARPTNLTDEFEFPIGTYL
NYECRPGYYGRPF3IICLKNSWTGAKDRCKRKSCRNPPDPVRGWYHYLKDIOFGSQI
KYSCTKGYRLIGSSSATCIISGDTYLMDNEFPLFDDRIPGGLPPTITNCDFISTNRENE
HYGSVVTYRCNPGSGGRKYFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV
ENGILYSDNRSLFSLMEVVEFRCQPGFVMKGPRVKCQALNKWEPELPSCSRVCQPPP
DVLHAERTQRDKDNFSFGAEVYDEFYCDEGFQLKGSSASYCVLAGMESLWNSSVPVCB
DFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCB
OIFCRMPPAILNGRHTGTPEGDIPYGKEISYACDTHDRGMTFNLIGESSIRCTSDPC
OIFCRMPPAILNGRHTGTPEGDIPYGKEISYACDTHDRGMTFNLIGHTSDPC
OIFCRMPPAILNGRHTGTPEGDIPYGKEISYACDTHDRGMTFNLIGHTSDPC
OIFCRMPPAILNGRHTGTPEGDIPYGKEISYACDTHDRGMTFNLIGHTSDPC
OIFCRMPPAILNGRHTGTPAILNGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAINGRHTGTPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CR1"
<1. .>1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CR1" :
51. .1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNGVWSSPAPRCELSVPAACPHPPKIQNGHDIGGHVSLYLPGMTISYICDPGYLLVGK
GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHYGDYVTLKCEDGYTL
EGSPPGOCQADDRWDPPLAKCTSRAHDALIVGTSSGTIFFILLIIFLSWIILKHRKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Godon_start=3
/product="complement receptor 1"
/protein_id="AAA51439.1"
/db_xref="GI:557727"
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/db_xref="taxon:9598"
/cell_line="EBV transformed"
/cell_type="B cell"
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5.043
94.118
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476 c 478 g 510 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CR1"
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                                                                                           from:
                                                                                                                                                                                                                                    Percent Identity:
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                                                                                              1985
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86.029
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ACCESSION
VERSION
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AUTHORS
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ORGANISM
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seq_documentation_block:
LOCUS CHPCR1WT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 TATTATGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 alCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 rSerAlaLysAspLysCysLysArgLysSerCysArgAsnProProAspP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCTGGCGGTTGTGGTGCTTGCGCTGCCGGTGGCCTGGGGTCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primary sequence of an alternatively spliced form of CR1. Canditor the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birmingham, D.J., Shen, X.P., Hourcade, D., Nickells, M.W. and Atkinson, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimpanzee complement receptor
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 153 (2), 691-700 (1994)
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                          /product="complement receptor 1"

                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CR1"
<1. .>6044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
DFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                            /gene="CR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 /codon_start=3
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type one (CR1) mRNA,
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: CHPCR1WT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TATTATGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 sAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThrAspA 52
aThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrProV 152
                                                                                                                                                                                    IleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSerAl 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rSerAlaLysAspLysCysLysArgLysSerCysArgAsnProProAspP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCTGGCGGTTGTGGTGCTGCTTGCGCTGCGGTGGCCTGGGGTCAATG
                                                                                                                                                                                                                                                                                              CTGTGAATGGCATGGTGCATGTGATCAAAGACATCCAATTCGGATCCCAA
                                                                                                                                                                                                                                                                                                                                                                    roValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlySerGln 118
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATCCTCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerValTrpTh 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTTGAGTTTCCCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATGCCCCAGAATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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FASPTIPINDEEFPVCTSLNYECREGYPGKMFSISCLENLYWSSYEDNCRKKSGGPPD
EPFNGMVHINTDTQFGSTVNYSCNEGFRLIGSPSTTCLYSGNNVTWDKKAPICEIIS
EPPPTISNGDEYSNNRASFHNCTVTYQCHTGFDGEQLFELVGERSIYCTSKDDQVGV
WSSPPPTGISTNKCTAPEVENAIRVPGNRSFFSLTEIVRFRCQPGFVMVGSHTVQCQT
NGRWGPKLPHGSRYCQPPPEILHGEHTPSHQDNFSPQEVFYSSEPGYDLRGAASLHC
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HTGKEPLEVFEPGKAVNYTCDEHEDDGTTFDLIGESTIRCTSDFQGNGVNSSEAERCGI
LGHCQAPDHELEAKLKYQTNASDFPIGTSLKYCERPEYYGRPESITCLDNLWGSFKD
VCRRKQKTPEDDFVNGMYVTTDIQVGSRINYSCTGHRLIGHSSAECLLDRLWGSFKD
VCRKSCKTPEDDFVNGMYVTTDIQVGSRINYSCTGHRLIGHSSAECHLOGUSAHWS
TKPPICQRIFPGLANGDFISTNRENFHYGSVTYRCNLGSRGKVFELVGEPSI
YCTSNDDQVGIWSGPAPQCIIPNKCTFPNVENGILVSDNRSLFSLNEVVEFRCQPGFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIFCPSPPVIPNGRHTGKPLEVFPFGKÅVNYTCDPHPDRGTTFDLIGESTIRCTSDPQ
GNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYKCRPEYYGRPFS
ITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHS
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HCVLAGMKALWNSSVEVCEQIFCPNPPAILNGRHTGTPFGDIFYGKEISYACDTHPDR
GMTFNLIGESSIRCTSDPQGNGVWSSPAPRCELSVPAACPHPPKIQNGHDIGGHVSLY
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YDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRVLFPLNLQLGAKVSEVCD
EGFRLKGSSVSHCVLVGMRSLMNNSVPVCEQIFCPNPFAILNGHTGTPFGDIPYGKE
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LNEVVEEFKCOPGFANKGPRYKKOALIKWEPELPSCSEVCOPPDVLHAEKTORDKDK
ESPGQEVEYSCEPGYDLRGAASIKCTPOGDWSPAAPTCEVKSCDGPMGQLLNGRYLFP
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KVYHYGDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRAHDALIVGTSSGTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENEHYGSVVTYRCNPGS
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106 69

56

9

ORIGIN BASE COUNT

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REFERENCE
AUTHORS
TITLE
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ACCESSION
alignment_block:
US-10-031-904-8 x HSCR1RS
                                                                                                                                                                                                             BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr:HSCR1RS
                                                                                                                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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::|||||
                                                                                                                                                                                                                                                                              polyA_site
                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                   sig_peptide
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Submitted (29-NOV-1988) Hourcade D., Howard Hughes Medical
Institute, 660 S. Euclid St. Louis Mo, 63110, USA
2 (bases 1 to 2376)
1 Hourcade, D., Miesner, D.R., Atkinson, J.P. and Holers, V.M.
Identification of an alternative polyadenylation site in the human
C3b/C4b receptor (complement receptor type 1) transcriptional unit
and prediction of a secreted form of complement receptor type 1
J. Exp. Med. 168 (4), 1255-1270 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3. Exp. 1
89010527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CR1 mRNA for C3b/C4b receptor secreted X14362 Y00812 X14362.1 GI:30197
                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence overlaps with that reported by Klickstein et. al. in J. Exp. Med. 165:1095-1112(1987) x05309 and in J. Exp. Med. 168:1699-1717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternate splicing; C3b/C4b receptor; complement receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hourcade, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor.
                                                                                           Ratio:
                                                                                                                                                                                                                                   633 a
                                                                                                                                                                                                                                                                                /product="mature CR1 receptor (AA 1-543); secreted form" 2376
                                                                                                                                                                                                                                                                                                                                                                                             DVLHAERTORDKDNFSPGOEVFYSCEPGYDLRGAASMRCTPOGDWSPAAPTCEVKSCD
DFMGOLLNGRVLFPVNLOLGAKODFVCDEGFOLKGSSASYCVLAGMESLWNSVSVPVCE
OIFCPSPPVI FUNGRHTGKEVLEVFPSGKAVNYTCDPHDDRGTSFDLIGESET IRCTSDPO
GNGVWSSPAPRCGILGHCOAPDHFLFAKLKTOTNASDEPIGTSLKYECRPEYYGRPFS
                                                                  644.50
5.035
94.118
                                                                                                                                                                                                                                 /note="polyA site"
549 c 568 g
                                                                                                                                                                                                                                                                                                                                                                            ITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRINYSCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYECRPGYSGRPFSIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQI
KYSCTKGYKLIGSSSATCIISGDTVIWDUSTPPLCDRLFCGLPFTITNGDFISTNRRNF
HYGSVDTYTRONGSGGRKVFELVGESGIYCTSNDDQVGINSGPAPQCIIPNGCTPPNV
ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA32541.1"
/db_xref="G1:736240"
/translation="SLLAVVVLLALPVAWGQCNAPEWLPFARPTNLTDEFEFPIGTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     base in codon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CR1-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="HL-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haplotype="CR1-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                       Percent Identity:
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                                                                                                                    Length:
                                                                                           Gaps:
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                                                                       86.029
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_sts:G28591
                                                                                                                                                                                                                        COMMENT
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TRSION
TYWORDS
                                                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                     OURCE
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CACATGCATCATCTCAGGTGATACTGTCATTTGGGATAATGAAACACCTA 405
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| CTGCTGGCGGTTGTGGTGCTGCTTGCGCTGCCGGTGGCCTGGGGTCAATG
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                                                                                                                                                                                                                                                                                                                                     human STS SHGC-35372, sequence tagged site. G28591
                                                                                                                                                            Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157255687
                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2376)
                                                                                                                                                                                                                                                                                                              G28591.1 GI:1408406
STS; STS sequence; primer; sequence tagged site
                                                                              Primer A: TGAGTTGGCAGCAACATCTC
Primer B: CATACTCTTATATGTGCACTGCCC
STS size: 216
PCR Profile:
                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                     4157259689
                                                                                                                                        myers@shgc.stanford.edu
Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
                                               Denaturation:
                                                                      Initial incubation:
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BASE COUNT
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US-10-031-904-8 x G28591
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Taq Polymerase:
Total Vol:
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/db_xref="taxon:9606"
/map="1"
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25 ng
each 1 uM
each 200 uM
: 0.05 units/ul
10 ul
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Prepared with primer pairs provided by Sandoz, derived -- Washington University/Merck EST sequence.
Location/Qualifiers from X14362

Gaps: 1 Percent Identity: 86.029

20 LeuLeuAlaAlaLeuValLeuLeu...LeuSerSerPheSerAspGlnCy CTGCTGGCGGTTGTGGTGCTGCTTGCGCTGGCGTGGCCTGGGGTCAATG 55

52 89 105

106 AGTTTGAGTTTCCCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGT

85 205

85 rSerAlaLysAspLysCysLysArgLysSerCysArgAsnProProAspP 102 |:::|||||||||||| 206 TGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATCCTCCAGATC 255

118 305

355

aThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysThrProV 152 CACATGCATCATCTCAGGTGATACTGTCATTTGGGATAATGAAACACCTA

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DEFINITION ACCESSION VERSION
                                       seq_documentation_block:
LOCUS A86601
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AUTHORS
TITLE
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US-10-031-904-8 x A86593
                                                                         seq_name: gb_pat:A86601
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LOCUS A86593
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|CCCAAATTAANTATTCTTGTACTAAAGGTTACCGTCTGATTGGTTCCTCC 303
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           Sequence 10 from Patent A86601
A86601.1 GI:6735175
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Smith, R.A. and Cox, V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
Patent: WO 9839433-A 2 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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Sequence 2 from Patent WO9839433.
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/db_xref="taxon:32644"
159 c 148 g 15
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Gaps: 0
Percent Identity: 90.909
                       591 bp
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REFERENCE
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US-10-031-904-8 x A86601
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|CCCAANTAAANATTCTTGTACTAAAGGTTACCGTCTGATTGGTTCCTCC 303
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||GGACTGGTGCTAAGGACCGTTGCCGACGTAATCTTGTCGTAATCCGCC 203
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3M unidentified
unclassified.

E 1 (bases 1 to 591)
S Smith, R. A. and Cox. V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
L Patent: WO 9839433-A 10 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GE
LOCATION/QUALIFIERS
                                                                                                                                                                                                                       rProValCysAsp 154
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1 (bases 1 to 591)
Smith, R.A. and Cox, V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
                                                       unidentified unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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                                          unclassified
                                                                                            A86603.1 GI:6735176
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/db_xref="taxon:32644"
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LOCUS A86605
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Ratio:
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Sequence 14 from Patent WO9839433.
A86605
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SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
LOCALLION/QUALIFIERS
                                                                              Smith, R.A. and Cox, V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
Patent: WO 9839433-A 14 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
                                                                                                                                                          unidentified unclassified.
                                                                                                                                                                                            unidentified.
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158 c 146 g
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      /organism="unidentified"
/db_xref="taxon:32644"
160 c 149 g 15
                                                                 Location/Qualifiers
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KEYWORDS
SOURCE
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US-10-031-904-8 x A86605
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                                                       alignment_scores:
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                                                                                                                  BASE COUNT
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             Percent Similarity:
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Ratio:
                                                                                                                                                                                    unclassified.

1 (bases 1 to 591)

Smith,R.A. and Cox,V.F.
SMITH,R.CARPOR TYPE 1 (CR1)-LIKE SEQUENCES
PATENT; WO 9839433-A 16 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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Sequence 16 from Patent WO9839433.
A86607
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                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
160 c 151 g 15
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Length: 121
Gaps: 0
Percent Identity: 90.909
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PAT 21-JAN-2000

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VERSION
KEYWORDS
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US-10-031-904-8 x A86609
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LOCUS A86609
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US-10-031-904-8 x A86607
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ACCESSION
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Percent Similarity:
                                Align seg 1/1 to: A86609
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34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
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                                                                                                                                                                                                                                                                          UNLIASSIFIED.

1 (Dases 1 to 591)

Smith,R.A. and Cox,V.F.

COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
Patent: WO 9839433-A 18 11-SEP-1998;

PATENT RICHARD ANTONY GODWIN (GB); ADPROTECH PLC

LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A86609 591 bp
Sequence 18 from Patent WO9839433.
                                                                                                                                                  Quality:
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Gaps: 0
Percent Identity: 90.909
                                to: 591
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67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83

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alignment_block:
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LOCUS AR029199
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Percent Similarity:
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                                                      50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP
               50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP
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TGATGAATTTGAGTTCCCGATCGGTACCTACCTGAACTACGAATGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33 from patent US 5859223.
AR029199
                                                                                                                                                                                                                 Quality:
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Mossakowska,D.Ewa.Irena., Dodd,I., Freeman,A.Mary. and
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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161 c 150 g
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Gaps: 0
Percent Identity: 90.909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGACTGGTGCTAAGGACCGTTGCCGACGTAAATCTTGTCGTAATCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATCCGGTTAACGGCATGGTGCATGTGATCAAAGGCATCCAGTTCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCGATTTGTGAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAAATTAAATATTCTTGTACTAAAGGTTACCGTCTGATTGGTTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The baboon erythrocyte complement receptor is a glycophosphatidyl inositol-linked protein encoded by a homologue of the human CRI-like genetic element unpublishes a force
  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio cynocephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement C3b; complement receptor; glycophosphatidylinositol-linked protein. Papio cynocephalus cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L77977.1 GI:1301608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papio cynocephalus complement L77977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BABCORE
                                                                                                  413
                                                                                              DLRGAASLHCTPQGDWNPEAPICTVKSCDDFLGQLPHGRVLFPLNLQLGAKVSFVCDE
GFRLKGRFASHCYLAGKKALWNSSVPVCEQIFCDNPPALLNGRHIGAPLGDIFYGKEV
SYICDPHPDRGMTVNLIGESTIRCTSDPQGNGVWSSPAPRCELSVPAGANDALIVGTL
SGTIFVLLFIIFLS"
4 427 c 411 g 437 t
                                                                                                                                                                                            WGQCNAPEQLPFARPTNLTDASEFPYGTYLKYECLPGYHGKPFSIICLKNSVWTSAKD
KCTRKSCRNPKDPVNGWYHVIKDIQFGSQINYSCNKGYRLIGSSATCIISGNTYIWD
NETPICEIIPGLPFTIANGDFISTSREYFPYGSVYTYKCNLGSGRKKLFELVGEPSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="bone marrow"
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                                                                                                                                                                                                                                                                                                                                                                            /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                              /note="homologue of human CR1-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Papio cynocephalus"
/db_xref="taxon:9556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="erythrocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1688
                                                                                                                                                                                                                                                                                                                                                                                                                         . 157
    .50
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  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor mRNA, partial
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    138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                              genetic element"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                                       JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr:BABCR1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-031-904-8 x BABCORE
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                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ProGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVa
|||||||||
| 1|| CCTGGTTATCATGGAAAACCATTTTCTATCTATCTGCCTAAAAAACTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 SerGlnileLysTyrSerCysProLysGlyTyrArgLeuileGlySerSe 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AAGATCCTGTGAATGGCATGTGCATGTGATCAAAGACATCCAGTTCGGA
                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 hrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 roAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 CTGGACAAGTGCTAAGGACAAGTGCACACGTAAATCATGTCGTAATCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 TCAATGCAATGCCCCGGAACAGCTTCCATTTGCCAGGCCTACCAACCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 pGlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 GGATCCCTGTTGGCGGTTGTGGTGCTGCTCGCGCTGCCGGTGGCCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GlyLeuLeuAlaAlaLeuValLeuLeu...LeuSerSerPheSerAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCTATTTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCAAATTAATTATTCTTGTAATAAAGGATACCGACTCATTGGTTCCTC
                                                                                                                                                                                                                                                                                                                                   C3b/C4b complement component receptor; complement component receptor CRI; complement receptor 1. Papio hamadryas (clone SPC-CYT3NC) cDNA to mRNA. Papio hamadryas
                                                                                                                                                                                                                                   Clemenza, L.,
                                                                                                                                                                                                                                                     Cercopithecinae; Papio.
1 (bases 1 to 6000)
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     complete cds
L39791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papio hamadryas complement component receptor type
                                                                                                                                                                         Unpublished (1995)
                                                                                                                                                                                              Primary sequence of the baboon
                                                                                                                                                                                                                Atkinson, J.P
                                                                                                                                                                                                                                                                                                                                                                                                                L39791.1 GI:662828
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1..6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.874
89.130
                                                                                                                                       1. .6000
/gene="CR1"
                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                   Subramanian, B.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from:
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Percent Identity: 81.159
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                                                                                                                                                                                                                                   Nickells, M.W.,
                                                                                                                                                                                                200 kDa
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339

289 83 239 99 189 ű

389 116

mRNA

linear

1 (CR1) mRNA, PRI 11-FEB-1995 489 150 439

C3b/C4b receptor (CR1)

Hourcade, D.E.

CDS

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alignment_scores:
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ORIGIN
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BABCR1A from: 1 to: 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lignment_block:
US-10-031-904-8 x BABCR1A
                                                                                                                                                               101 TTGATGAGCCTGAGTTTTCCATTGGGACACATCTGAAGTATGAATGTCGC
                                 67 ProGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVa 83
                                                                                                                                                                                                     50 hrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArg 66
                                                                                                                                                                                                                                                                                                                          51 TCAATGCAATGCCCCGGAACAGCTTCCATTTGCCAGGCCTACTGAACTAA 100
                                                                                                                                                                                                                                                                                                                                                                    33 pGlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 GlyLeuLeuLeuAlaAlaLeuValLeuLeu...LeuSerSerPheSerAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGATCCCTGCTGGCGGTTGTGGTGCTCGCGCTGCCGGTGGCCTGGGG 50
CCTGGTTATTATGGAAGACCATTTTCTATCATCTGCCTAAAAAACTCAGT 200
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WSPAAPRCEVKSCDSLGQLPWGRVLFPRSLQLGAK VDEVCDEGFQLKGGSASYCVLA
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LIGESTIRCTSDPQGNOVWSSRAPRCGILGHCKAPDHFLFAKLKTQTNASDFPIGTSL
KYECRPEYYGKPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRI
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GROWMSSPAPRCELSVRAGHCKTPEQFFPASPTIPINDFEFFRGGENGTWTWGCH
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89.130
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LSPLNLQLGAKVSFVCDEGFRLKGRSASHCVLAGMKALWNSSVPVCEQIFCPNPPAIL
NGRHTGTPLGDIPYGKEVSYTCDPHPDRGMTFNLIGESTIRCTSDLQGNGVWSSPAPR
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WYHVITDIQVGSRINYSCTTGHRLIGHSAECVTSGHTAHWSTERPICQRIPGLPPP
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PQCIIPNKCMPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWE
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GPRRVQCQALNKWEPELPSCSRVCQPPPDVLHGERTQRDKDIFQTGQEVFYICEPGYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRWDPPLAICTSRARDALIVGTLSGMIFVILFIIFLSWIILKYRKGNNAHEKPKEVAI
HIHSQGGSSVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELSVPAACPHPPKIQNGHYIGGHVSLYLPGMTIGYICDPGYLLVGKGIIFCTDQGIW
SQLDHYCKEVNCSFPQFMNGISKELEMKKVYHYGDYVTLECEDGYALEGSPWSQCQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="acts as C3b/C4b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTCDPHPDRGMTFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCKAPDHFLFAKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="complement component receptor type
/protein_id="AAA62170.1"
/db_xref="GI:662829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRGAASLRCTPQGDWSPAAPRCEVKSCDDSLGQLPNGRVLFPRSLQLGAKVDFVCDEG
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Percent Identity: 78.986
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Search information block:
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9b_est1:Ai7361375
9b_est1:Ai7361375
9b_est1:Ai7361375
9b_est2:Bi79335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est2:BE552138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: Oct 9, 2002 6:07 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM of: US-10-031-904-8 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -Q-(ggn2_1)(USFTO_Spool)(USI(031904/runat_09102002_084256_23627/app_query.fasta_1.232
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-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p2n.model -DEV=xlh
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                                                   1268.30
1187.10
1083.91
1043.91
1044.41
819.205
814.39
814.39
812.47
812.47
812.47
805.75
877.92.21
799.12
799.63
779.23
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   3.4e-33

9.8e-33

1.8e-32

1.8e-32

1.8e-32

1.6e-32

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2.9e-31

4.2e-31

4.2e-31

4.7e-31

4.7e-31

1.7e-29

2.3e-28

4.5e-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8e-49
5.0e-45
2.2e-36
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1.4e-51
4.0e-51
                                                                                                                                                                                                                                                                                                                                                     .2e-35
2.9e-35
7.1e-35
3.7e-34
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2.7e-77
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1.6e-34
2.0e-34
2.6e-34
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4.1e-36
5.2e-36
5.3e-36
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     HESSELIA hw29d0.x1 NCI_CGAP_Ki
AI740881 qj94e04.x1 NCI_CGAP_Ki
AI718588 as46h01.x1 Barstead ac
BF240184 601905704F1 NIH_MCC_54
I AI7185459 at11h03.x1 Barstead ac
I BF240184 601905704F1 NIH_MCC_54
I AI735459 at11h03.x1 Barstead ac
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BE178335 601808574F1 NCI_CGAP_M
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BE156939 601774087F1 NCI_CGAP_LU
BE159845 601767506F1 NCI_CGAP_LU
BE159845 601765853F1 NCI_CGAP_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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LOCUS BE552138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BE552138
                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                    Align seg 1/1
                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
     49 uThrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysA 66
                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                           134
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gb_est2:BM488775
gb_est2:BM425702
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US-10-031-904-8 x BE552138/rev
BE552138
465 bp mRNA linear EST 10-AUG-2000 hw29d02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3184323 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMAN);, mRNA sequence.
BE552138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 456.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@image.llnl.gov
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE552138.1 GI:9793830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                                                 reverse of: BE552138
                                                                                                                                                                                                                  789.00
5.556
100.000
                                                                                                                                                                                                                                                                                                                                                                                /note=Torgan: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "39 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone="IMAGE:3184323"
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289.50
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Gaps: 0
Percent Identity: 100.000
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1.2e-24
2.6e-24
6.3e-22
6.9e-22
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i AM919879 ES7351183 Rat gene
i AA755782 vv65f64.rl Stratage
i BM488775 pgm2n.pk008.m6 worm
i BM425702 pgf2c.pk001.j17 Pri
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REFERENCE
AUTHORS
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LOCUS AI240881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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MMENT
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                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 lySerGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 GTCTGGACAAGTGCTAAGGACAAGTGCAAACGTAAATCATGTCGTAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 rolleHisSerAsnPheSerLeuGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AACACCTGTTTGTGACAGTGAGTTGAAATATGCATTCCTATTTCTTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 oProAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 ValTrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGTCTGCCACATGCATCATCTCAGGCAACACTGTCATTTGGGATAATAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATACATTCTAATTTTTCTCTGGAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerSerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLy 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCCCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAGATCCTGTGAATGGCATGGCACATGTGATCAAAGACATCCAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est1:AI240881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 bp mRNA linear EST 28-JAN-1999 al94e04.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867134 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Lint at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 625 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           High quality sequence stop: 373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI240881.1 GI:3836278
                                                                                                                                                                                                                                                                  Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 443)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
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                                                  REFERENCE
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LOCUS AI718588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
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                                                                                                                         ORGANISM
                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                         Homo sapiens
                                                                                                                                                                                                                    AI718588
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alignment_block:
US-10-031-904-8 x AI240881/rev
                                                                                                                                                                                                                                                                                                                                      DEFINITION as46h01.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2320273 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AI240881 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 rProValCysAspSerGluLeuLysTyrAlaPheLeuPheLeuLeuProI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 erGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 leHisSerAsnPheSerLeuGlu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 TCTGCCACATGCATCTCAGGCAACACTGTCATTTGGGATAATAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 SerAlaThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysTh 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 CCCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AGATCCTGTGAATGGCATGGCACATGTGATCAAAGACATCCAGTTCGGAT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 oAspProValAsnGlyMetAlaHisVallieLysAspIleGlnPheGlyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 TGGACAAGTGCTAAGGACAAGTGCAAACGTAAATCATGTCGTAATCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 CTGGTTATTCCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 TGATGACTCTGAGTTTCCCATTGGGACATATCTGAACTATGAATGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442° CAATGCAATGTCCGGAATGGGCTTCCATTTGCCAGGCCTACCAACCTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 TACATTCTAATTTTTCTCTGGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 ACCTGTTTGTGACAGTGAGTTGAAATATGCATTCCTATTTCTTTTACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
                                                                                                                                                                                                                                                          AI718588.1 GI:5035844
                                                                                                                                                                                                                                                                                                               PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified py773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748.00
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Gaps: 0
Percent Identity: 97.163
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BASE COUNT
ORIGIN
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JOURNAL
191
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                                                                                                                                                                                                                                                                                         341 CTGGTTATTCCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTC 292
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                                                                                                                                                                                                                                                                                                                                                                                 50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh
                                                                                                         erGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
                                                                                                                                                                                                                    TGGACTGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATCCTCC
                                                                                                                                                                                                                                                                                                           roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                                                                                                                                                                                                                                                                                                                                 TGATGAGTTTGAGTTTCCCCATTGGGACATATCTGAACTATGAATGCCGCC
                                                                     CCCAAATTAAATATTCTTGTACTAAAGGATACCGACTCATTGGTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST project Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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5.102
97.163
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/db_xref="taxon:9606"
/clone="IMAGE:2320273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult, age 64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Barstead aorta HPLRB6"
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Percent Identity: 90.780
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REFERENCE
AUTHORS
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KEYWORDS
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US-10-031-904-8 x BF240184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 CCCATTCTAATTTTTCTCTGGAA 20
                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llni.gov Plate: LLCM1034 row: h column: 01 High quality sequence stop: 544.
Location/Qualifiers
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF240184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4133424"
/clone_lib="NIH_MGC.54"
/clone_lib="NIH_MGC.54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/note="Oygan: bone marrow; Vector: pDNR-LIB (Clontech);
/note="Oygan: bone marrow; Vector: pDNR
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                                                                                                                                                                                                                                                                                                                           678.00
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Gaps: 3
Percent Identity: 88.957
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3E:4133424 5',
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FEATURES
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LOCUS BM477528
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                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 hrProValCys.....AspSerGluLeuLysTyr 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TGGGTTGCTTCTGGCGGC.CTGGTGTTGCTGCTGTCCTCCTTCTCCGATC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgPr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rSerAlaThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTC 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSe 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspProValAsnGlyMetAla.HisValIleLysAspIleGlnPhe.Gly 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCTGTGAATGGCATGGCACCATGTGATCAAAGACATCCAGTTCAAGA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACAAGTGCTAAGGACAAGTGCAAACGTAAATCATGTCGTAATCCTCCA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1063)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12272 row: n column: 04
                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
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BM477528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM477528.1 GI:18526570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM477528 1063 bp mrNA linear FAGENCOURT_6484929 NIH_MGC_85 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                    quality sequence stop:
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:554371"
/clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DHHUB (phage resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                            .1063
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le IMAGE:5554371
                                                                                                REFERENCE
                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                  KEYWORDS
                                                                           AUTHORS
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COMMENT

TITLE

SOURCE

VERSION

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seq_documentation_block:
LOCUS AI735459
                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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Ratio: 4.883
Percent Similarity: 89.865
                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 erglyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 GGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 ATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GGTGCTGCCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 IleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgPr 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGAC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                at11h03.x1 Barstead aorta HPLRE6 Homo sapiens cDNA clone IMAGE:2354837 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                          human.
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a 286 c 272 g 249 t 5 others
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COMMENT
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ORIGIN
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                 seq_name: gb_est2:T66824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AI735459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 CTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACCGTTTTCTATCAT 306
                                                                                                                                                                                                                                                                                                                                                                       255 AATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATGGCACATGTGATC 206
                                                                                             161 PheLeuPheLeuLeuProIleHisSerAsnPheSerLeuGlu 174
                                                                                                                                                                                                                                                                                                                                                                                             94 ysSerCysArgAsnProProAspProValAsnGlyMetAlaHisValIle 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LeuAsnTyrGluCysArgProGlyTyrSerGlyArgProPheSerIleI1 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 eCysLeuLysAsnSerValTrpThrSerAlaLysAspLysCysLysArgL 94
                                                                                                                                                         alileTrpAspAsnLysThrProValCysAspSerGluLeuLysTyrAla 160
                                                                                                                                                                                                                CCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCTCAGGCAACACTG
                                                                                                                                                                                                                                                                                                                LysAspIleGlnPheGlySerGlnIleLysTyrSerCysProLysGlyTy 127
                                                                                                                                      TCATTTGGGATAATAAAACACCTGTTTGTGACAGTGAGTTGAAATATGCA
                                                                                                                                                                                                                                                      rArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrV 144
                                                                                                                                                                                                                                                                                             AAAGACATCCAGTTCAGATCCCAAATTAAATATTCTTGTCCTAAAGGATA 156
                                                           TTCCTATTTCTTAAAAAGATACATTCTAATTTTTCTCTGGAA 14
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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314 286 1810
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5.432
97.368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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                                                                                                                                                                                                                                     alignment_block:
US-10-031-904-8 x T66824
                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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LOCUS T66824
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                                                                                                                20 uLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspGlnCysAsnV 37
37 alProGluTrpLeuProPheAlaArgProThrAsnLeuThrAspAspPhe 53
                                        74 TCTGGCGGCCCTGGTGTTGCTGCTGTCCTCCTCCCGATCAATGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 bp mRNA linear EST 07-MAR-1995 ya50b08.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:66327 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN);, mRNA sequence.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The Wasbu-Merck EST Project
Unpublished (1995)
Other_ESTs: ya50b08.s3.exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High qality sequence stops: 324 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                   Quality:
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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5.236
98.148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:66327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares fetal liver spleen 1NFLS"
                                                                                                                                                                                                                                                                                        Length: 108
Gaps: 2
Percent Identity: 97.222
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ACCESSION
VERSION
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 TGAATGGNATGGNACATGTG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 TCCCGGAATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGACTTT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 GluPheProIleGlyThrTyrLeuAsnTyrGluCysArgPro.GlyTyrS 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estéwatson.wustl.edu
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: -21M13LR
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                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: ya50b08.r3.exp
Contact: Wilson RK
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Mammalia; Eutheria;
1 (bases 1 to 389)
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314 286 1810
         /clone="IMAGE:66327"
/clone_lib="Soares fetal liver spleen lNFLS"
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/db_xref="taxon:9606"
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COMMENT
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US-10-031-904-8 x T66823/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 GCATCATCTCAGGCAACACTGTCATTTGGGATAATAAAACACCTGTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 ATANTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACAT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 sTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSerAlaThrC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AsnGlyMetAlaHisValI1eLysAspI1eGlnPheGlySerGlnI1eLy 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 CTAAGGACAAGTGCAAACGTAAATCATGTCGTAANCCTCCAGANCCTGTG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 GACAGTGAGTTGAAATATGCATTCCTATTTCTTTTACCGATACATTCTAA
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Email: est@watson.wustl.edu
Insert Size: 791
High quality sequence stops: 300 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                          .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
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541 bp mRNA linear EST 16-MAR-1995 yd41a11.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA cJone IMAGE:110780 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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alignment_block:
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  405 TTCATTTGGGGGGTTATTAAAAACACCCGTTTTGTGGACAGTNGAGTTTG 454
                                    144 lileTrpAspAsn.....LysThrProValCys......AspS 155
                                                                              355 CATTGGGTTTCCTCGTCTTGCCACATGGCATTCATTTCAGGGCAACATTG 404
                                                                                                                     128 ArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrVa 144
                                                                                                                                                               305 GTTTCGGATTCCCAAATTTAAATATTCTTGTTCCTAAAGGGNTACCGANT 354
                                                                                                                                                                                                    114 nPheGly...SerGInIleLysTyrSerCys.ProLysGly.....Tyr 127
                                                                                                                                                                                                                                            255 CCTCCAGATCCTGTGAATGGGCATGGCACATGTGGATTCAAAGACATCCA 304
                                                                                                                                                                                                                                                                                                                             205 AGTCTGGACAAGTGCTAAGGACAAGTGCAAACGTNAAATCATGTCGTAAT 254
                                                                                                                                                                                                                                                                                                                                                                                                            155 CGCCCTGGTTATTCCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 TAACTGATGACTTTGAGTTTCCCCATTGGGACATATCTGAACTATGAATGC
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                                                                                                                                                                                                                                                                     99 ProProAspProValAsn.GlyMetAlaHisVal..IleLysAspIleGl 114
                                                                                                                                                                                                                                                                                                                                                    82 rValTrpThrSerAlaLysAspLysCysLysArg.LysSerCysArgAsn 98
                                                                                                                                                                                                                                                                                                                                                                                                                                   66 ArgProGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 euThrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 rAspGlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PheProGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSe 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 CGATCAATGCAATGTCCCGGAATGGCTTCCATTTGCCAGGCCTACCAACC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 300. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 791 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
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80.233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:110780"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares fetal liver spleen lnFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:466397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532.00
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                                                        alignment_scores:
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                                                                                                                                         BASE COUNT
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                      Quality:
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ORIGIN

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seq_name: gb_est2:H73873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502 TTTNCTC 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 eSerLeu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 GAANTATGGCNTTCCCATTTTCCTTT...TTACCNATTACATTTTATTT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 erGluLeuLysTyrAlaPheLeuPheLeuLeuProIle.HisSerAsnPh 171 :: ::: ||| ||| ||||||||||| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H73873

440 bp mRNA linear EST 31-OCT-1995
ys14d08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:214767 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
1 PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Insert Size: 706
High quality sequence stops: 275
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 706 Std Extor: 0.00
Seg primer: MJ3RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiases, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, B., Moore, B., Morits, M., Parsons, J., Prange, C., Rifkin, L., Rhlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
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            83 a
quality sequence stop: 275.
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:214767"
                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism≕"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares fetal liver spleen INFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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Ratio:

4.560 92.373

Percent Identity: 88.983 Length:

497.00

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 CTGTGGATTGGGCATNGGCACATTGTNGATCAAAAGGACATT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 TGCTAAGGACAAGTGCAAACGTTAAATCATGTTCGTAATCCTTCCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 TCCCGGAATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGACTTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GAGTTTCCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGGTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 TCTGGCGGCCCTGGTGTTGCTGCTGCTCCTCCCGATCAATGCAATG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 roValAsn.GlyMetAlaHisValIle.....LysAspIle 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 rAlaLysAspLysCysLysArg.LysSerCys.ArgAsnPro.ProAspP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 CCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGGACAAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 erGlyårgProPheSerIleIleCysLeuLysAsnSerValTrp.ThrSe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GluPheProIleGlyThrTyrLeuAsnTyrGluCysArgPro.GlyTyrS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 alProGluTrpLeuProPheAlaArgProThrAsnLeuThrAspAspPhe 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 CCCGTCCGTCTCGAGCGTCCCTTTCCTTCCCGGCGCTTTCCTGGGTTGCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 uLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspGlnCysAsnV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ProValArgLeuGluArgProPheProSerArgArgPheProGlyLeuLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 601)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oul pp mRNA linear EST 31-JAN-199: mu80g07.rl Stratagene mouse melanoma (#937312) Mus musculus cDNA clone IMAGE:651900 5' similar to gb:M23529 Mus musculus complement receptor (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                       Seq primer: -28m13 rev1 ET from Amersham
                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA212152.1 GI:1810867
                                                                                                                                                                                                                                                                  MAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nouse mouse
                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:651900"
/clone_lib="Stratagene mouse melanoma (#937312)"
                                                                                                                                                   Location/Qualifiers
                                                                                                                            . 60
                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Louis, MO 63108
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VERSION
KEYWORDS
  REFERENCE
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                                                                                       SOURCE
                                                                                                                                                     ACCESSION
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Ratio: 3.754
Percent Similarity: 78.322
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                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                              469 ATTGGGATACTGAGGCACCCATTTGTGAG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AspIleGlnPheGlySerGlnIleLysTyrSerCysProLysGlyTyrAr 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 CAAACAAGACTCAACCTGGACGAGTGCTGAAGATAAGTGTATACGAAAAC 318
                                                                                                                                                                                                                                                                                                                                                                    145 leTrpAspAsnLysThrProValCysAsp 154
                                                                                                                                                                                                                                                                                                                                                                                                                 419 CCTCATTGGTTCCTCCTCTGCTGTATGTGTCATCACTGATCAAAGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 gLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrValI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 GGCATTCAGTTTGGATCCCGTATTAATTATACTTGTAATCAAGGATACCG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 AATGTAAAACTCCTTCAGATCCTGAGAATGGCTTGGTACATGTACACACA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 TTGTATGAATGTCTCCCAGGATATATCAAGAGGCAGTTCTCTATCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 AACCTATAAATCTAACTGATGAATCCATGTTTCCCATTGGAACATATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 erCysArgAsnProProAspProValAsnGlyMetAlaHisValIleLys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AsnTyrGluCysArgProGlyTyrSerGlyArgProPheSerIleIleCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 AGCCTTCGGCGGGGAGGAGTCAAGCTAGAAGTTTTGCTGCTGTTCTTGCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 SerArgArgPheProGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSe 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 rSerPheSer...AspGlnCysAsnValProGluTrpLeuProPheAlaA 45
                                                                                                                                                          577 bp mRNA linear EST 26-JaN-:
H3013A12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3013A12 5', mRNA sequence.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 577)
                                                                  Mus musculus
                                                                                     house mouse.
                                                                                                                                BG077250.1 GI:12559818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 143
Gaps: 1
Percent Identity: 55.245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                   EST 26-JAN-2001
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COMMENT

TITLE

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alignment_block:
US-10-031-904-8 x BG077250
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                                                                                                                                                                                                                                                                   122 GGAGTCAAGCTAGAAGTTTTGCTGCTGTTCTTGCTGCCATTTACTTTGGG 171
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                                                                                                                                                  172 TCACTGCCCAGCCCCATCACAGCTTCCTTCTGCCAAACCTATAAATCTAA 221
                                                                                    50 hraspaspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArg 66
                                                                                                                                                                               33 pGlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuT 50 :::||| :::||| :::||| | |||||||||
                                                                                                                                                                                                                                                                                                                       18 GlyLeuLeuAlaAlaLeuValLeuLeuSerSerPheSer...As 33
                                CTGATGAATCCATGTTTCCCATTGGAACATATTTGTTGTATGAATGTCTC 271
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This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. plate: H3013 row: A column: 12 Seg primer: -2LM13 Reverse
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Other_ESTs: H3013A12-3
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Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 577 POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) rot primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000, proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, bevelopment, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex
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Mo}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; This
clone is among a rearrayed set of 15,247 clones from 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.805
79.710
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/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
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/strain="C57BL/6J"
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/db_xref="taxon:10090"
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                                                          alignment_scores:
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Quality:
Ratio:
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Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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plate: LLAM11946 row: a column: 10
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                                                                                                                                                                               163
                                                                                                                                                                        Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 146 c 158 g 191 t
                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                           /tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
418.50
3.805
                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5371665"
/clone_lib="NCI_CGAP_Mam2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
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US-10-031-904-8 x BI697900
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                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 795)
11 (bases 1 to 795)
11 (MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                     DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11634 row: i column: 18 High quality sequence stop: 795.
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BI455761
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                    Location/Qualifiers
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6
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musculus cDNA clone IMAGE:5251289 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451
                                                                                                                                       seq_documentation_block: LOCUS BI078162
                                                                                                                                                                                                      seq_name: gb_est2:B1078162
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                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                  150 hrProValCysAsp 154
                                                                                                                                                                                                                                                     CACCTATTTGTGAG 553
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house mouse
                                                                   BI078162
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Align seg 1/1 to: BI455761 from: 1 to: 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 CCAGGATATATCAAGAGGCAGTTCTCTATCACCTGCAAACAAGACTCAAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TCACTGCCCAGCCCCATCACAGCTTCCTTCTGCCAAACCTATAAATCTAA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 rSerAlaThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 TCCCGTATTAATTATACTTGTAATCAAGGATACCGCCTCATTGGTTCCTC 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 lTrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProP 100 :|||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 ProGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVa 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 hraspaspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArg 66
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BI078162.1 GI:14496492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5251289"
/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/strain="C57/B6"
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Percent Identity: 55.797
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REFERENCE
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US-10-031-904-8 x BI078162
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285 CTGGACGAGTGCTGAAGATAAGTGTATAACAATGTAAAACTCCTT 334
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                                                                                        CAGATCCTGAGAATGGCTTGGTACATGTACACACAGGCATTCAGTTTGGA 384
                                                                                                                 roAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 116
                                                                                                                                                                                                                                                                                                       ProGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVa 83
                                                                                                                                                                                                                                                                                                                                                                                                  hrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArg 66
TCCCGTATTAATTATACTTGTAATCAAGGATACCGCCTCATTGGTTCCTC
                           SerGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSe 133
                                                                                                                                                                                                                                                                                    CCAGGATATATCAAGAGGCAGTTCTCTATCACCTGCAAACAAGACTCAAC
                                                                                                                                                                                                                                                                                                                                                                               CTGATGAATCCATGTTTCCCCATTGGAACATATTTGTTGTATGAATGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Plate: LLAM11042 row: o column:
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Location/Qualifiers
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/clone_lib="NCI_CAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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Percent Identity: 55.797
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Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
Search time (sec): 41.920000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
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-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPECL-0.000
-LOOPEXT-0.000 -GAPOP-4.500 -GAREXT-0.050 -XGAPOP-10.000
-XGAPEXT=0.000 -FGAPOP-4.500 -FGAPEXT-7.000 -YGAPOP-10.000
-XGAPEXT-0.500 -EGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELXET-7.000 -START-1
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-USER-US10031904_@CGN1_168 -NCPU-6 -ICPU-3 -LONGLOG
-USER-US10031904_@CGN1_168 -NCPU-6 -ICPU-3 -LONGLOG
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                                                                                                                                     1134 | 1134 | 2116 | 2134 | 2234 | 1365 | 3 860 | 1 969 | 1 2096 | 2 2096 | 2 2096 | 2 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 | 1 2096 |
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;Patent No. 5256642
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                                                                                                                                                                                                                                                    AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy
                                                                                                                                                                                                                                                                                                                                                                                                           ysCysLysArgLysSerCysArgAsnProProAspProValAsnGlyMet 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProPheProSerArgArgPhe.....ProGlyLeuLeuAlaAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS 140
                                                                                                                                                                                                   GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG
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4.883
89.865
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from: 1 to: 6951

169

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56

219

123

419

369

319

73

269

469

Gaps: 2
Percent Identity: 81.757

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TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR 1 (CR1) AND A THROMBOLTIC AGENT, AND THE USE THEREOF
                                                                                                                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILLING DATE: 26 SEP-1989
APPLICATION NUMBER: 332,865
FILLING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILLING DATE: 01-APR-1988
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                 us/08/588,128
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;Patent No. 5472939
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TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: 5472939-1 from: 1 to: 6951
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
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                                                                                                                                      107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
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420 TACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCT 469
                                                    123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleS 140
                                                                                                         370 GTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTG 419
                                                                                                                                                                                                                     320 GGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATG 369
                                                                                                                                                                                                                                                                                                                           270 GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACA 319
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                                                                                                                                                                                                                                               73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 IleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgPr 73
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Ratio:
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alignment_block: US-10-031-904-8 x US-08-769-967A-33
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                                                                                                                                                                                                         Align seg 1/1 to: US-08-769-967A-33 from: 1
                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (610) 270-50 INFORMATION FOR SEQ ID NO
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: King, William T.
REGISTRATION NUMBER: 30,
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APPLICATION NUMBER: 08/440,569
FILING DATE: 15-May-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Freeman, Anne Mary TITLE OF INVENTION: Soluble CR1 Derivatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
                                                         57 TGATGAATTTGAGTTCCCGATCGGTACCTACCTGAACTACGAATGCCGCC 106
                                                                             50 rAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP
                                                                                                                                                                    34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh
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CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                  7 CAGTGCAACGCTCCGGAATGGCTGCCGTTCGCGCGCCCGACCAACCTGAC 56
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CLASSIFICATION: 536
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Ratio:
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P.O. Box 1539
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Dodd, Ian
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Gaps: 0
Percent Identity: 90.909
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;Patent No. 5256642
                                                                                                                                                                                                                                                                                          alignment_block:
US-10-031-904-8 x 5256642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                        5256642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; RECEPTOR 1
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TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5256642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-APR-1988
SEQ ID NO:3:
                                                                                                                                                                                                                                                          Align seg 1/1 to: 5256642-3
                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                        gnment_scores:
                                                               2761
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APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THEREOF
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                                                                                                                                                   44 aArgProThrAsnLeuThrAspAspPheGluPheProIleGlyThrTyrL 61
                                                                                              61
                              78
                                                                                                                                                                                                                       28 LeuSerSerPheSerAspGlnCysAsnValProGluTrpLeuProPheAl 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 332,865 FILING DATE: 03-APR-1989 APPLICATION NUMBER: 176,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 412,745 FILING DATE: 26-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
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ACCGATTTGTGAC
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                                                               TGAATTATGAATGCCGTCCTGGGTATTTTGGGAAAATGTTCTCTATCTCC 2810
                                                                             euAsnTyrGluCysArgProGlyTyrSerGlyArgProPheSerIleIle 77
               CysLeuLysAsnSerValTrpThrSerAlaLysAspLysCysLysArgLy 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CR1) AND A THROMBOLTIC AGENT, AND THE METHODS
                                                                                                                                                                                                                                                                                                                                                                           Quality:
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4.250
81.890
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APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG, WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5472939-3
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CHERENT APPLICATION NUMBER: US/08/138,825

FILING DATE: 19-OCT-1993

PRIOR APPLICATION NUMBER: 588,128

APPLICATION NUMBER: 588,128

APPLICATION NUMBER: 412,745

FILING DATE: 24-SEP-1990

APPLICATION NUMBER: 412,745

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332,865

FILING DATE: 01-APR-1988

FILING DATE: 01-APR-1988

FILING DATE: 01-APR-1988

FILING DATE: 01-APR-1988

ED ID NO:3:
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                                                                                                                                                                                                                               2661 CTTTCTGTTCGTGCTGGTCACTGTAAAACCCCAGAGCAGTTTCCATTTGC
                                                                            2811
2861 ATCATGTGGACCTCCACCAGAACCCTTCAATGGAATGGTGCATATAAACA 2910
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                                                                                                                                                                                                                                                                                                                                                 LeuSerSerPheSerAspGlnCysAsnValProGluTrpLeuProPheAl 44
                             sSerCysArgAsnProProAspProValAsnGlyMetAlaHisVallleL 111
                                                                          TGCCTAGAAAACTTGGTCTGGTCAAGTGTTGAAGACAACTGTAGACGAAA
                                                                                               CysLeuLysAsnSerValTrpThrSerAlaLysAspLysCysLysArgLy
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-139-195-1
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                  alignment_block:
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US-10-031-904-8 x US-08-139-195-1
                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 07,
FILING DATE: 21-SEP-1992
PRIOR APPLICATION NUMBER: US 07,
FILING DATE: 21-JTT-1777
VTTORNEW / 777
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                                                                                                                                                                                                                                                                          TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Atkinson
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release *1 '
                                                                                                                                                                                                                                                                                                             LENGTH: 1545 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/139,195
FILING DATE: 20-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
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                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson,
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                                                                                                                                                                                                Human t-Cell Line HSB2
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                                                      291.00
2.853
60.714
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RECOMBINANTLY PRODUCED HUMAN MEMBRANE COFACTOR PROTEIN (MCP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
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                                                        Percent Identity: 40.476
                                                                                              Length:
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 uLeu 157
                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                         STREET:
  CLASSIFICATION:
                                                                                                                                                                                                                   Massachusetts
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-310-416A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08310416A Patent No. 5679546
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 20 or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/310,416A
APPLICATION NUMBER: US/08/310,416A
FILING DATE: 22-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JORE-LONG KO et al.
TITLE OF INVENTION: CHIMERIC PROTEINS WHICH BLOCK
TITLE OF INVENTION: COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 AAAGGATCAGTAGCAATTTGGAGCGGTAAGCCCCCAATATGTGAAAAGGT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 SerGlyAsnThrValIleTrpAspAsnLysThrProValCysAspSerGl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 AGTCCCTGCAAATGGGACTTACGAGTTTGGTTATCAGATGCACTTTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CCTGTGAGGAGCCACAA.....CCATTTGAAGCTATGGAGCTCATTGGT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 uAsnTyrGluCysArgProGlyTyrSerGlyArgPro.....PheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ArgProThrAsnLeuThrAspAspPheGluPheProIleGlyThrTyrLe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 lnCysAsnValProGluTrpLeuProPhe...........Ala 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 TGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTACTCCTTCTCCGATG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 oGlyLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACTATTTGTGATCGGAATCATACATGGCTACCTGTCTCAGATGACGCC 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAATGAGGGTTATTACTTAATTGGTGAAGAAATTCTATATTGTGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   225 Franklin Street
                                                                                                                                                    5.0)
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seq_documentation_block:
; Sequence 11, Applicati
; Patent No. 5851528

1, Application 5851528

US/08888171

GENERAL INFORMATION:

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; TYPE: nucleic acid
STRANDENNES: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-310-416A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Paul T. CLAIN REFERENCE/DOCKET NUMBER: 0618
REFERENCE/DOCKET NUMBER: 0618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                       151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 CCTGTGAGGAGCCA...... 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 olleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspAspPheGlu.....PhePr 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oGlyLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TTTGAAGCTATGGAGCTCATTGGTAAACCAAAACCCTACTATGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTTACTCCTTCTCCGATG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGAGCCTCCCGGCCGCCGAGTGTCCCTTTCCTTCCTGGCGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       ro......PheSerIleIleCysLeuLysAsnSerValTrpThrSer 86
                                     oValCysAspSerGluLeu 157
                                                                               CTATATTGTGAACTTAAAGGATCAGTAGCAATTTGGAGCGGTAAGCCCCC
                                                                                                                    AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
                                                                                                                                                                                               lnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSer 134
                                                                                                                                                                                                                                                                                     oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
                                                                                                                                                                                                                                                                                                                                  GTCTCAGATGACGCCTGTTATAGAGAAACATGTCCATATATACGGGATCC 317
                                                                                                                                                                                                                                                                                                                                                                     ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
AATATGTGAAAAGGTTTTG 486
                                                                                                                                                              AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT
                                                                                                                                                                                                                                                TTTAAATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 267
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Percent Identity:
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-888-171-11
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US-10-031-904-8 x US-08-888-171-11
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Quality:
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                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-888-171-11 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REGISTRATION NUMBER: 0618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEPHONE: 617/542-890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jone-Long, Ko
APPLICANT: Higgins, Paul J.
APPLICANT: Yeh, C. Grace
TITLE OF INVENTION: METHODS OF INHIBITING COMPLEMENT
TITLE OF INVENTION: ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-JUL-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                     104
                                                                                                                                  34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                         54 TGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTACTCCTTCTCCGATG 103
                                                                                                                                                                                                                17
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                               4 ATGGAGCCTCCCGGCCGCCGCGAGTGTCCCTTCCTTCCTGGCGCTTTCC
                                                                                                                                                                                                                                                                          1 MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                   oGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
                                                                  AspAspPheGlu.....
                               .....TTTGAAGCTATGGAGCTCATTGGTAAACCAAAACCCTACTATGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02110-2804
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                                                              .....PhePr 56
                                                                                                                                                                                                                                                                                                                             to: 903
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: 6
: 39.884
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; Sequence 1, Application US/08793418C
.; Patent No. 6130062
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US-10-031-904-8 x US-08-793-418-1
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APPLICANT: The Austin Research Institute
TITLE OF INVENTION: Improvements in Production
FILE REFERENCE: CALA-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-793-418-1
                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-793-418-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/793,418C CURRENT FILING DATE: 1997-02-25 EARLIER APPLICATION NUMBER: PCT/AU95/00553 EARLIER FILING DATE: 1994-08-30 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: sequence with wild type SCR
-08-793-418-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1134
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AlaThrCysIleIleSerGlyAsnThrVallleTrpAspAsnLysThrPr 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 oValCysAspSerGluLeu 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 TTTAAATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC 367
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                                                                              51 TGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTACTCCTTCTCCGATG 100
34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                         17 oGlyLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
                                                                                                                                                                                                                       1 MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oIleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                                ATGGAGCCTCCCGGCCGCCGCGAGTGTCCCTTCCTTCCTGGCGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ro......PheSerIleIleCysLeuLysAsnSerValTrpThrSer 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                         289.00
2.890
57.803
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 6
Percent Identity: 39.884
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6
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: subSCR3 variant US-08-793-418-3
                            alignment_block:
                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-793-418-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: The Austin Research Institute
TITLE OF INVENTION: Improvements in Production
FILE REFERENCE: CALA-100
CURRENT APPLICATION NUMBER: US/08/793,418C
CURRENT FILING DATE: 1997-02-25
US-10-031-904-8 x US-08-793-418-3
                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08793418C Patent No. 6130062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/AU95/00553 EARLIER FILING DATE: 1994-08-30
                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1134
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAGGATACTTCTATATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AATATGTGAAAAGGTTTTG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 TTTAAATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 GTCTCAGATGACGCCTGTTATAGAGAAACATGTCCATATATACGGGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 .....TTTGAAGCTATGGAGCTCATTGGTAAACCAAAACCCTACTATGA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 CCTGTGAGGAGCCA...... 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AspAspPheGlu.....PhePr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT 414
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                                                                                                                                      Quality:
                                                                                                            Ratio:
                                                                                289.00
2.890
57.803
                                                                                Percent Identity: 39.884
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Align seg 1/1 to: US-08-793-418-3 from: 1

to: 1134

MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr 17

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5846715

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
DEPLICANT: PURCELL, Damian F. J.
APPLICANT: MCKENZIE, Jan F. C.
APPLICANT: MCKENZIE, Ian F. C.
TITLE OF INVENTION: CD46 VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSE: FOLEY & Lardner
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W.,
                                                                                 FILING DATE: 11-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AATATGTGAAAAGGTTTTG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 TTTANATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CCTGTGAGGAGCCA......120
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GTCTCAGATGACGCCTGTTATAGAGAAACATGTCCATATATACGGGATCC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAGGATACTTCTATATAC 214
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                          APPLICATION NUMBER: PCT/
FILING DATE: 10-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                          FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/528,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20007-5109
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5846715
                                                       PCT/AU91/00199
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alignment_block:
US-10-031-904-8 x US-08-528-057-41
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; LOCATION:
US-08-528-057-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-528-057-41 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
135 AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
                                           447 AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT 496
                                                                                                                                  397 TTTAAATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC 446
                                                                                                                                                                        102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
                                                                                                                                                                                                                    347 GTCTCAGATGACGCCTGTTATAGAGAAACATGTCCATATATACGGGATCC 396
                                                                                                                                                                                                                                                                                                      297
                                                                                                                                                                                                                                                                                                                                                                                        247 GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAAGGATACTTCTATATAC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 ....TTTGAAGCTATGGAGCTCATTGGTAAACCAAAACCCTACTATGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 CCTGTGAGGAGCCA...... 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (2. 904136
                                                                                                                                                                                                                                             87 ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
                                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                                                                                                                                                                                                                                                                               56 olleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AspAspPheGlu.....PhePr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 oGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ATGGAGCCTCCCGGCCGCCGAGTGTCCCTTTCCTTCCTGGCGCTTTCC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                    InIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSer 134
                                                                                                                                                                                                                                                                                                   CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 346
                                                                                                                                                                                                                                                                                                                                        ro.......PheSerIleIleCysLeuLysAsnSerValTrpThrSer 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)672-5399
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185..1192
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2.890
57.803
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FR: 17227/112 DACO
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alignment_block: US-10-031-904-8 x US-08-528-057-45
                                                                                                                                                                   ; LOCATION: US-08-528-057-45
                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-528-057-45
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK0133/90
FILING DATE: 11-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227/112 DACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08528057 Patent No. 5846715
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INFORMATION FOR SEQ ID NO:
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APPLICANT: RUSSELL,
APPLICANT: MCKENZIE,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,686
FILING DATE: 11-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Petentin Release #1.0, Version #1.25
                                                                                                                                                                                                                         LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1304 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00199
FILING DATE: 10-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CONCUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                   1304 base pairs
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MCKENZIE, Ian F. C.
WENTION: CD46 VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                mat_peptide
196..1065
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CONCURRENTLY HEREWITH
                                                      289.00
2.890
57.803
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                                                      Percent Identity:
                                                                                           Length:
                                                      39.884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-458-084-3
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                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         APPLICANT: Fodor, William L
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
                 OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch,
COMPUTER: Dell 486/50
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M
                                                                                                                                                                                                                                                          TITLE OF INVENTION: Chimeric Complement TITLE OF INVENTION: Inhibitor Proteins NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458
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                                                                                                                              ZIP:
                                                                                                                                                             CITY: Fairfield
STATE: Connecticut
 APPLICATION NUMBER:
                                                                                                                                               COUNTRY:
                                                                                                                                                                                                  STREET:
                                                                                                                              06430
                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08458084
                                                                                                                                                                                                1951 Burr Street
                                                                                                                                               USA
                                                                                                                                                                                                                     Maurice M. Klee
US/08/458,084
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750 Kb storage

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to: US-08-528-057-45
 from: 1 to: 1304
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135 AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
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                                                                151 oValCysAspSerGluLeu 157
                                                                                                                                                                                                                                                                                                                                                                                                                       408 TTTAAATGGCCAAGCAGTCCCTGCAAATGGGACTTACGAGTTTGGTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GTCTCAGATGACGCCTGTTATAGAGAAACATGTCCATATATACGGGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAGGATACTTCTATATAC 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 olleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AspAspPheGlu.....PhePr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 oGlyLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 ATGGAGCCTCCCGGCCGCCGAGTGTCCCTTTCCTTCCTGGCGCTTTCC 143
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                                                                                                                                                                                                                                                                               AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT
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AATATGTGAAAAGGTTTTG 576
                                                                                                                                       CTATATTGTGAACTTAAAGGATCAGTAGCAATTTGGAGCGGTAAGCCCCC
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CLASSIFICATION:

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US-08-458-084-3
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US-10-031-904-8 x US-08-458-084-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MCP (CD46) full length cDNA
"""POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens PUBLICATION INFORMATION: AUTHORS: Lublin, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-120
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                        164
                                                                                                                                                51
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VOLUME: 168
PAGES: 181-194
DATE: 1988
                                                                                                                                                                                   34
                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                  44 ATGGAGCCTCCCGGCCGCCGAGTGTCCCTTCCTTCCTGGCGCTTTCC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                   1 MetAlaProProValArgLeuGluArgProPheProSerArgArgPhePr 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                   olleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgP 73
                                                                                                                                                                                 lnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
                                                                                                                                                                                                                                           oGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAGGATACTTCTATATAC 257
                                                                                                 AspAspPheGlu.....PhePr 56
                                                                                                                                                                                                                           TGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTACTCCTTCTCCGATG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Atkinson, J.P.
Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for Inclusion
in the Multi-Gene Family of
Complement-Regulatory Proteins.
                                                                         TTTGAAGCTATGGAGCTCATTGGTAAACCAAAACCCTACTATGA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arce, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liszewski, M.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Journal of Experimental Medicine
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2.890
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Percent Identity: 39.884
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-205-508-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Patent No. 5627264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-1400
                                                                                                                                                                                                                                                                           TELEFAX: (203) 254-1101 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: Dell 486/50
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 oValCysAspSerGluLeu 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 CTCCTCTTGCCACCCATACTATTTGTGATCGGAATCATACATGGCTACCT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Chimeric Complement
TITLE OF INVENTION: Inhibitor Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
                                                          HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 ro.....PheSerIleIleCysLeuLysAsnSerValTrpThrSer
PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
                                                                                                                           MOLECULE TYPE: cDNA to mRNA DESCRIPTION: MCP (CD46) full length cDNA
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                          TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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                                          ORGANISM:
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Liszewski, M.K.

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alignment_block:
US-10-031-904-8 x US-08-205-508-3
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; PAGES: 181-194
; DATE: 1988
US-08-205-508-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                          oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
                                                                                      CTATATTGTGAACTTAAAGGATCAGTAGCAATTTGGAGCGGTAAGCCCCC
                                                                                                                              AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
                                                                                                                                                                            AGATGCACTTTATTTGTAATGAGGGTTATTACTTAATTGGTGAAGAAATT 457
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AATATGTGAAAAGGTTTTG 526
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Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for Inclusion
in the Multi-Gene Family of
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Arce, M.A.
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alignment_scores:
 Quality:
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289.00 2.890

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seq_documentation_block:
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US-08-482-148-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (203) 772 3655
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4 mb storage
COMPUTER: IBM compatible (Pentium)
OPERATING SYSTEM: Windows 95 under MS DOS
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Terminal Complement
TITLE OF INVENTION: Inhibitor Fusion Genes and Proteins
NUMBER OF SEQUENCES: 17
COPPRESSIVE - 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (203) 776 1790
VOLUME: 100
PAGES: 181-194
DATE: 1988
                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
AUTHORS: Liszewski,M.K.
                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                   AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 6/07/9
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STATE: Connecticut
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                                                                                                        TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
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                                                                                        TITLE:
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                                                                    JOURNAL:
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                                                                                      Complement-Regulatory Proteins.
                                                                                                  : Atkinson, J.P.

Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for Inclusion
in the Multi-Gene Family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1530 base pairs
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Arce, M.A.
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Lemons, R.S.
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                                                                    Journal of Experimental Medicine
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                 151 oValCysAspSerGluLeu 157
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208 GATTGGTGAACGAGTAGATTATAAGTGTAAAAAAGGATACTTCTATATAC 257
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:*
2: gb_htg:
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627
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Copyright (c) 1993 - 2000 Com
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ALIGNMENTS	G28591 G28591 G28691 G2BCRLX CHPCRLWT BABCOREA BABCOREA BABCOREA G25967 G27827 CHPCRLY A86693 A86603 A86605 A86607 A86609 AR029199 AR029199 AR029115 RAF512 RAF512 RAF512 RAF512 RAF512 RAF512 RAF512 HUMCPLA D4211.5 G27828 MUSCRYL GERRP MUSCRYL GERRP MUSCRYL GERRP MUSCRYL GAL137789 HUMCRL102 HUMCRL103 HUMCRL104 HSMCP06 HSMCP07 HSMCP06 HSMCP07 HSMCP07 HSMCP08	AX078362 HSCR1
	05000000000000000000000000000000000000	78362 Sequence 816 Human mRNA

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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
VERSION
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AX078362
    BASE COUNT
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                                                                                                                                                        JOURNAL
                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                        AUTHORS
                                                                                     Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 627)
Au-Young, J., Bandman, O., Tang, Y.T., Yue, H., Azimzai, Y., Burford, N.,
Baughn, M.R., Lu, D.A., Hillman, J.L., Patterson, C. and Lal, P.
Baughn, M.R., Lu, D.A., Hillman, J.L., Patterson, C. and Lal, P.
Receptors and associated proteins
Patent: WO 0107612-A 30 01-FEB-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AX078362 627 bp
Sequence 30 from Patent W00107612.
AX078362.1 GI:13158031
                                                                                                                                                                                                                                                                                                                                    human.
    142 a
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/db_xref="taxon:9606"
/note="Incyte ID No: 103561CB1"
/note="173 c 128 g 184 t
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  Klickstein, L.B., Bartow, T.J., and Fearon, D.T.
                           Direct Submission
Submitted (20-OCT-1988) Klickstein L.B.,
725 N. Wolfe St., Baltimore, MD 21205
2 (bases 1 to 1531)
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                             C3b/C4b complement component receptor; C3b/C4b receptor; CD35 antigen; complement receptor; glycoprotein; membrane protein.
                                                                                 Klickstein, L.B
                                                                                                                                      Homo sapiens
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            Miletic, V.,
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type 1 (CR1,
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SLWNSSYPVCEQIFCCSPPVLFNGRYTGKPLEVFFFKAKLWYTCDPHDRGTSFDLIG
ESTIRCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
ECRPEYYGFFSITCLINLWSSPKDVCKRKSCKTPDDFVNGMYHYITDLQVGSRLHYS
CTTGHRLIGHSSAECILSGNTAHWSTKFPICQRIPGGLFPTIANGDFISTNRENFHYG
SVYTTRCNLGSRGRKVEELVGEPSIYCTSNDDQVGIWSGPAPQCIIFNKCTPPNVENG
ILVSDNRSLFSLNEVVEERCQPGFVNGFRRVYCQALMKWEPELFSCSRVCQPPEIL
HGEHTPSHQDNFSPGQEVFYSCEPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFL
GQLLHGRVLEFLNLQLGAKUSFVCDREGFRLKGSSVSHCVLVGNHSLWNSVFVCHHF
CPNPFAILNGRHTGTPSGDIPYGKEISYTCDPHDDRGMTFNLIGESTIRCTSDPHGNG
VWSSPAPRCELSVRAGHCKTPEQFPRASFTIPINDFEFFVGTSLHYECREGFTGKNES
ISCLENLWSSVEDNCRKSCGGPPERFFNGMYHINTDTQFGTSTUNYSCNEGFRLIGSP
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/note="long

2851. .4209

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LTEIIRFRCQPGFVMYGSHTVQCQTNNGWGFKLHCSRVCQPPEPILIGEHTLISHQDN
FSPGQEVFYSCEPSYDLFRGAASLHCTPQGDWGFKLHCSRVCQPPEPILIGEHTLISHQDN
FSPGQEVFYSCEPSYDLFRGAASLHCTPQGDWGFAFRCTVKSCDDFLGQLFHBRYLLF
LNLQLGAKVSFVCDEGFRLKGRSASHCYLAGMKALWNSSVPVCEQIFCPNPPAILNGR
HTGTPPGDIPYGKEISYACDTHPDRGMTFNLLGESSIRCTSDPGGNGVWSSPAPRCEL
SVPAACPHPPKLQNGHYIGGHVSLYLPGMTISTTCDPGYTLYGKGFIFCTDQGIWSQL
DHYCKEVNCSFPLFMMGISKELEMKKYYHYGDYVTLKCEDGYTLEGSFWGQCQADDRW
DPLAKCTSRAHDALIVGTLSGTIFFILLIIFLSWIIILKHRKGNNAHENPKEVAIHLH
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GDFISTNERWFHYGSVVTYRCNPGSGGRKVFELVGESTCTSUDDQVGIWSGPAPQC
IIPMCTPPNVENGILVSDNRSLFSLMEVVEFRCOPGFVMKGFRRVKCQALNKWEPEL
PSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSP
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DPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQT
NASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDYCKRKSCKTPPDPVNGMYH
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RVKCQALNKWEPELPSCSRVCQPPDDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRG
AASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQL
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/clone_lib="lambda S2T (ATCC #37546)."
28. .150
28. .6147
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APEWLPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKDRCRRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGACAG 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tttgagtttcccattgggacatatctgaactatgaatgccgccctggttattccggaaga 302
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                                                                                                                              The sequence overlaps with that reported by Klickstein et. J. Exp. Med. 165:1095-1112(1987) x05309 and in J. Exp. Med 168:1699-1717(1988).
                                                                                                                                                                                                                Hourcade, D., Miesner, D.R., Atkinson, J.P. and Holers, Y.M. Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CR1 mRNA for C3b/C4b receptor secreted form. X14362 Y00812 X14362.1 GI:30197
                                                                                                                                                                                                                                                                                 Submitted (29-NOV-1988) Hourcade D., Howard Hughes Medical Institute, 660 S. Euclid St. Louis Mo, 63110, USA 2 (bases 1 to 2376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alternate splicing; C3b/C4b receptor; complement receptor;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                 Exp. Med. 168 (4), 1255-1270 (1988)
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/db_xref="taxon:9606"
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/haplotype="CR1-A"
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                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                               /organism="Homo sapiens"
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REFERENCE
AUTHORS
JOURNAL
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SOURCE
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Best Local
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                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2376)
                                                                                                                                                                          human STS SHGC-35372,
G28591
               Unpublished
                                  Myers, R.M.
                                                                                                                                       STS; STS sequence; primer; sequence tagged
                                                                                                                                                         G28591.1
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DVLHAERTORDKDNFSPGQEVFYSCEPGYDLKGAASHRCTPQGDWSPAAPTCEVKSCD
DFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLANSSVPVCE
QIFCPSPPVLPNGRHTGKFLEVFPFGKAVNYTCDPHDDRGTSFDLIGESTIRCTSDPQ
GNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFS
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/db_xref="GI:736240"
/db_xref="GI:736240"
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KYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPFTTNGDFISTNRENF
KYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPFTTNGCFIFPNV
HYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTFPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="mature CR1 receptor (AA 1-543);
2376
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549 c 568 g
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Contact: Richard M. Myers

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    FEATURES

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primer_bind
BASE COUNT 63
ORIGIN
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Best Local :
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TTAAATATTCTTGTACTAAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCA
             ttaaatattcttgtcctaaaggataccgactcattggttcctcgtctgccaccatgcatca
                                                    ctccagatcctgtgaatggcatggcacatgtgatcaaggacatccagttcggatcccaaa
                                                                                                              TAAAAAACTCAGTCTGGACTGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATC
                                                                                                                           taaaaaactcagtctggacaagtgctaaggacaagtgcaaacgtaaatcatgtcgtaatc
                                                                                                                                                                    CATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACCGTTTTCTATCATCTGCC
                                                                                                                                                                                   ATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATTTGAGTTTGAGTTTTCCCATTGGGA 126
                                                                                                                                                                                                                                                      aatggcttccatttgccaggcctaccaacctaactgatgactttgagtttcccattggga 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepared with primer pairs provided by Sandoz, derived from X14362 -- Washington University/Merck EST sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer B: CATACTCTTATATGTGCACTGCCC STS size: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer A: TGAGTTGGCAGCAACATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                            633 a
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PCR Cycles:
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549 c 568 q 6
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/db_xref="taxon:9606"
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90.5%;
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262 catatctgaactatgaatgccgccctggttattccggaagaccgttttctatcatctgcc 321
                                                                                                             202
                                                                                                                                                                            142 tgcttctggcggccctggtgttgctgctgttctcccttctccgatcaatgcaatgtcccgg 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 TCTCAGGTGATACTGTCATTTGGGATAATGAAACACCTATTTGTGACAG 415
                                                                    67
                                                                                                                                                     7 TGCTGGCGGTTGTGGTGCTGCTTGCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAG 66
                                                                                        aatggcttccatttgccaggcctaccaacctaactgatgactttgagtttcccattggga 261
                                                                    AATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCCATTGGGA 126
                                                                                                                                                                                                                                            368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative splicing product; complement receptor Pan troglodytes cDNA to mRNA. Pan troglodytes
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J. Immunol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 1985)
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                                                                                                                                                                                                                                       Similarity 90.0
58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    521
                                                                                                                                                                                                                                                                                                                                                                       þ
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CR1"
51. .1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPPRVKCQALNKWEPELPSCSRVCQPPP
DVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASLRCTPQGDWSPATFTCEVKSCD
DFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCYLAGMESLMNSSVFYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYECRPGYYGRPFSIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKDIQFGSQI
KYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENF
HYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon;9598"
/cell_line="EBV transformed"
/cell_type="B cell"
                                                                                                                                                                                                                                                                                                                                                                  /product="complement receptor 1"
476 c 478 g 510 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GF1FCTDQG1WSQLDHYCKEVNCSFPLFMNG1SKELEMKKVYHYGDYVTLKCEDGYTL
EGSPWSQCQADDRWDPPLAKCTSRAHDALIVGTSSGT1FF1LL1IFLSWI1LKHRKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAHEKPKEVAIHLHSQGGSSVHPRTLQTNEENSRVLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIFCPNPPAILNGRHTGTPFGDIPYGKEISYACDTHPDRGMTFNLIGESSIRCTSDPQ
GNGVWSSPAPRCELSVPAACPHPPKIQNGHDIGGHVSLYLPGMTISYICDPGYLLVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="complement receptor 1"
/protein_id="AAA51439.1"
/brotein_id="AAA51479" .
/translation="SILAVVVLLALPVAWGQCNAPEWLPFARPTNLTDEFEEFPIGTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CR1"
<1. .>1985
                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CR1"
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                                                                                                                                                                                                                                                         Score 343.4; DB 9; Pred. No. 4.9e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHPCR1WT 6044 by Chimpanzee complement receptor L24920
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                                                 TITED A TOTAL OF THE CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="complement receptor 1"
/protein_id="AAA51438.1"
/db_xref="GI:557725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
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MKGPHRVKCQALNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSCEPG
YDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRVLFPLNLQLGAKVSFVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CR1"
/codon_start=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAAAACTCAGTCTGGACTGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCAGATCCTGTGAATGGCATGGTGCATGTGATCAAAGACATCCAATTCGGATCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368;
                                                                                                                                                                                                                   1688 bp mRNA linear [Papio cynocephalus complement receptor mRNA, partial L77977.1 GI:1301608
       The baboon erythrocyte complement receptor is a gly inositol-linked protein encoded by a homologue of t CRI-like genetic element
                                                                                                                                                          complement C3b; complement receptor; glycophosphatidylinositol-linked pro Papio cynocephalus cDNA to mRNA. Papio cynocephalus
                                                                Cercopithecinae; Papio.
1 (bases 1 to 1688)
Birmingham, D.J., Logar,
Unpublished
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FASPIT PINDEEP POGTSLINV SCREEK SKRESISCILERILVWSSYEDUCKRKSGGPP EPFNGMVHINTDTQFGSTVNY SCNEGFRLIGSPSTTCLYSGNNYTWDKKAPICELISC EPFNGMVHINTDTQFGSTVNY SCNEGFRLIGSPSTTCLYSGNNYTWDKKAPICELISC EPFNTISNGDFYSNNRASFHNGTVVTYQCTTGBPDGQLFELVGERSIYCTSKDDQVGV WSSPPDRCISTNKCTAPEVENALRYPGNRKSFESLTEIVRERCQPGFYMVGSHTVQCQT NGRWGPKLPHCSRVCQPPPEILHGEHTPSHQDNWSPPQOEPTYSCCEPGYDDLRGAASLHC TPQGDMSPEAPRCTVKSCDDFLCQLPHGRVIFPNLYQLGAKVSFVCDEGFRLKGRSAS TPQGDMSPEAPRCTVKSCDDFLCQLPHGRVLFPNLYQLGAKVSFVCDEGFRLKGRSAS HCVLAGMKALWMSSYPVCEDIFCPNPPALLINGRHTGTPFGDIPYGKEISTACDTHDDR GMTFNLIGESSIRCTSDPQGNGVWSSPAPRCELSVPAACHPPKLQNGHBIGGHVSLY LPGMTISYICDFGYLLVGKGFIFCTDQGTWSSPAPRCELSVPAACHPPKLQNGISKELEMK KVYHVGDYTLKCEGGTVESSPWSQCQADDRWDPPLAKCTSRAIDALTVGTSGTIF FILLIIFLSWIILKHRKGNNAHEKPKEVAIHLHSQGGSSVHPRTLQTNEENSRVLP" 61 a 1496 c 1462 g 1525 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISYTCDPHPDRGMTFNLIGESTIRCTSDPHGNGVWSSPAPRCELPVHAGHCKTPEQFP
   (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.8%;
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Pred. No. 6.2e-90;
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                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                        a glycophosphatidyl of the human
                                                                                                                                                                                                                                                                                                                                                                                         415
                                                                                                                                                                                                                                                                                                                                                                                                                         550
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Focus

FEATURES

source

/organism="Papio cynocephalus" /db_xref="taxon:9556" /cell_type="erythrocyte"

Location/Qualifiers

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Db
                                                                                                                     BABCR1A
LOCUS
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                                                              ACCESSION
                                                                                                   DEFINITION
                          KEYWORDS
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Best Local S
Matches 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASE COUNT
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CDS
                                                                                                                                                                                                                   493
                                                                                                                                                                                                                                                                                                                                                                                                       418
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                                                                                                                                                                                                                                                                                          433
                                                                                                                                                                                                                                                                                                                                                                                                                                        478 gttcctcgtctgccacatgcatcatctcaggcaacactgtcatttgggataataaaacac 537
                                                                                                                                                                                                                                                                                                                                                                   373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 gaagaccgttttctatcatctgcctaaaaaactcagtctggacaagtgctaaggacaagt 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 ATGCATCTGAGTTTCCCCGTTGGGACATATCTGAAGTATGAATGCCTCCCTGGTTATCATG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 atgactttgagtttcccattgggacatatctgaactatgaatgccgccctggttattccg 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 cttcccggcgctttcctgggttgcttctggcgccctggtgttgct---gctgtcctcct 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 GAAAACCATTTTCTATCATCTGCCTAAAAACTCAGTCTGGACAAGTGCTAAGGACAAGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 TCCTCTTCTGCTGCGGAGGATCCCTGTTGGCGGTTGTGGTGCTGCTCGCGCTGCCGGTGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AGAGAATGGGGGCCTCTTCTCCAAGAAGCCCGGAGCCGGTTGGGCCCGCCGCCGCCCGTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTATTTGTGAGA 504
                                                                                                                                                                                                                                                                                                                                                                                   aagacatccagttcggatcccaaattaaatattcttgtcctaaaggataccgactcattg 477
                                                                                                                                                                                                                                                                                        GTTCCTCGTCCGCCACATGCATCATCTCAGGCAATACTGTCATTTGGGATAATGAAACAC 492
                                                                                                                                                                                                                                                                                                                                                                 AAGACATCCAGTTCGGATCCCAAATTAATTATTCTTGTAATAAAGGATACCGACTCATTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397;
C3b/C4b complement component receptor; complement component receptor CR1; complement receptor 1.
                                                            Papio hamadryas complement component receptor complete cds. L39791
                                                                                                                     BABCR1A
                                        L39791.1 GI:662828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="VVLQRMGASSPRSPEPVGPPAPRLLFCCGGSLLAVVVLLALPVA MGQCNAPEQLFEARTINLTDASEFPVGTYLKYECLEGYHGKPESICLKNSVMTSAKD KCTRKSCRNPKDPVGMVHVIKDIQFGSQINYSCNKGYLGESSATCIISGNTVTHOL NETPICEIIPCGLPFTIANGDFISTSREYFPYGSVVTYRCNLGSGRKKLFELVGEPSI YCTSKDDQVGIWSGPAPQCIIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQPGFV MKGPRHVQCQALNKWEPELPSCSRVCQPPPEILHGEHTPSHQDFSPGQEVFYSCEPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYICDPHPDRGMTVNLIGESTIRCTSDPQGNGVWSSPAPRCELSVPAGANDALIVGTL
SGTIFVILFIIFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLRGAASLHCTPQGDWNPEAPICTVKSCDDFLGQLPHGRVLFPLNLQLGAKVSFVCDE
GFRLKGRFASHCVLAGMKALWNSSVPVCEQIFCPNPPAILNGRHIGAPLGDIPYGKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="complement receptor"
/protein_id="AAA99004.1"
/db_xref="GI:1301609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="bone marrow"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="homologue of human CR1-like genetic element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 328.8; DB 9
Pred. No. 9.5e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 g
                                                                                                                     dq 0009
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                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1688;
                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                 type 1 (CR1) mRNA,
                                                                                                                   PRI 11-FEB-1995
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142 tgcttctggcggccctggtgttgctgctgctcctccttctccgatcaatgcaatgtcccgg

8 TGCTGGCGGTTGTGGTGCTCGCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCGG

67

Matches Query Match

353;

Conservative

Loca1

Similarity

51.0%;

score 320; DB 9;
Pred. No. 4.9e-83;
0; Mismatches 55

55;

0;

Gaps

0

Length 6000; Indels

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
ORIGIN
                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primary sequence of the baboon 200 kDa C3b/C4b receptor (CR1) Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papio hamadryas (clone SPC-CYT3NC) cDNA to mRNA. Papio hamadryas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemenza, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atkinson, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 6000)
                                  1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRRVOCOALNKWEPELPSCSRVCOPPPDVLHGERTQRDKDTG7GGEVFY1CEPGYE
LRGAASLRCT9OGDWSPAAPRCEVKSCDDSLGGLPNGRVLFPRSLQLGAKVDFVCDEV
FQLKGSSASYCVLAGMESLWNSSVPVCEQ1FCPSPPV1PNGRHTGKPLEVFPFGKAVT
                                                                                                                                                                  LSPLNLQLGAKVSFVCDEGFRLKGRSASHCVLAGMKALWNSSVPVCEQIFCPNPPAIL
NGRHTGTPLGDIPYGKEVSYTCDPHPDRGMTFNLIGESTIRCTSDLQGNGVWSSPAPR
CELSVPAACPHPPKIQNGHYIGGHVSLYLPGMTIGYICDPGYLLVGKGIIFCTDQGIW
                                                                                                                                                                                                                                                                        GSPSTTCLVSGNNUTWDKEAPICEIISCKPPPTISNODPYSNNHTSFHSGTVVTYQCH
TGPDGEQLFELVGERSIYCTSKDDQVGAWSSPPPRCISTAPEVKNGIRPGNRS
FFSLMEIVRFRCOPGFWNVGSHTVQCQTNNRWGPKLPHCSRVCQPPPEILHGEHTPSH
ODKFSPGQEVFYSCEPGYDLRGAASLHCTPQGDWSPEAPICTVKSCDEFLGQLPHGRV
                                                                                                                                                                                                                                                                                                                                                                                                                    HIPCPNPAALNGRHTGALLGDIPYGKEISYTCDPHADRGWFHLIGESTIRCTSOLO
GNGYWSSPAAPCELSVRAGHCKTPEOGPFFASSTIPINDFEPVGTSLNYECHPGYFGR
MFSISCLENLYWSSVEDNCRRKSCGTPPEPFNGWVHINTDTQPGSTYNYSCNEGFRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWEPELPSCSRVCQPPP
EILHGEHTPSHQDKFSPGQEVFYSCEPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCD
DFLGQLHHGRVLVPFNLQLGAKVSFVCDEGFRLKGSSVSHCYLVGMASLWNNSVPVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYECRPEYYGKPESITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRI
NYSCTTGHRLIGHSSAECIISGNTAHWSTKPPICQRIPCGLPPPIANGDFISTNREYF
HYGSVVTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPAPQCIIPNKCMPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSPAAPRCEVKSCDDSLGQLPNGRVLFPRSLQLGAKVDFVCDEGFQLKGSSASYCVLA
GMESLWNSSVPVCEQ1FCPSPPV1PNGRHTGKPLEVFPFGKAVTYTCDPHPDRGMTFD
L1GEST1RCTSDPQGNGVWSSRAPRCG1LGHCKAPDHFLFAKLKTQTNASDFP1GTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IANGDFISTNREYFHYGSVVTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPA
PQCIIPNKCMPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLEWSSPKDVCKRKSCKTPPDPVNG
MYHVITDIQVGSRINYSCTTGHRLIGHSSAECVTSGNTAHWSTKPPICQRIPCGLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPICEKISCGLPPTIDNGDFFSANKEYFHYGSVVTYRCNLGSGGRKLFELVGEPSIYC
TSNEDQVGIWSGPAPQCIIPNKCTPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMK
                                                                                                  DRWDPPLAICTSRARDALIVGTLSGMIFVILFIIFLSWIILKYRKGNNAHEKPKEVAI
                                                                                                                                           SQLDHYCKEVNCSFPQFMNGISKELEMKKYYHYGDYVTLECEDGYALEGSPWSQCQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELPSCSRVCQPPPDVLHGERTQRDKDIFQPGQEVFYICEPGYDLRGAASLRCTPQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C3b/C4b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Papio hamadryas"
/db_xref="taxon:9557"
/clone="SPC-CYT3NC"
/cell_line="26CB-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="complement component receptor type 1"
/protein_id="AAA62170.1"
/db_xref="GI:662829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTCDPHPDRGMTFDLIGESTIRCTSDPQGNGVWSSPAPRCGILGHCKAPDHFLFAKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268. .>6000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MVHVIKDIQFGSQINYSCTEGHRLIGSSSATCIISGNTVIWDNE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="putative"
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Papio cynocephalus cDNA to mRNA.
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Papio cynocephalus
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1. (bases 1 to 945)
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     Conservative
                                                                                                                              /db_xref="GI:1301611"
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RKLFELVGEPSIYCTSNEDQVGIWSGPAPQCIIPNKCTPPNVENGILVSVNRSLFSLN
EVVEFRCQPGFYMKGFRRVQCQALNKMEPPELFSCSRVCQPPDDVLHGERTQRDXDIFQ
                                                                                                                                                                                                                                                                                                     /cell_type="lymphocyte"
/tissue_type="bone marrow"
/dev_stage="adult"
<1. .>945
<1. .>945
                                                                                                    TGQEVFYICEPSYDLRGAASLRCTPQGDWSPAAPRCEVK"
224 c 228 g 239 t 2 other
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/protein_id="AAA99005.1"
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                                                                                                                                                                                                                                                                                      /note="homologue of human CR1-like genetic element"
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/db_xref="taxon:9556"
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                 50.5%;
Score 316.8; DB 9;
Pred. No. 2.9e-82;
2; Mismatches 29;
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                                                                                                                                                                                Primer A: CC/
Primer B: CTC
STS size: 125
PCR Profile:
                                                                                                                                                                                                                                                                        Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Re Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900 Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G25967.1 GI:1348199
STS; STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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                                                                         Protocol
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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             Template: 10 ng
primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul
                                                                                                     Annealing: 56 degrees Polymerization: PCR Cycles: 35
                                                                                      Thermal Cycler:
                                                                                                                                                    Denaturation:
                                                                                                                                                                Presoak:
                                                                                                                                                                                                                                                          thudson@genome.wi.mit.edu
                                                                                                                                                                                                              CCAGAGAAAAATTAGAATGTATCGG
CTCGTCTGCCACATGCATC
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Best Local Similarity 95.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAGANCCTGTGAATGGCATGGCACATGTGATCAAAGACATCCAGTTCGGATCCCAAA
                                                          Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                        G27827

human STS SHGC-33387, sequence tagged site.
G27827
Primer A: CCAGAGAAAAATTAGAATGTATCGG
Primer B: CTCGTCTGCCACATGCATC
STS size: 125
                                                                                                                      Contact: Richard M. Myers
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
Myers,R.M.
                                                                                                                                                                                                                              G27827.1 GI:1396546
STS; STS sequence; primer; sequence tagged site.
                                                                                                                                               Unpublished
                                                                                                                                                                                                           Homo sapiens
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KCl: 50 mM
Tris-HCL: 10 mM
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                                                myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from dbEST (genbank accession T66823).
Location/Qualifiers
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/db_xref="taxon:9606"
/map="890.2 cR from top of Chrl linkage group"
25...149
25...49
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67 c 92 g
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 Mismatches

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primer_bind
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              345;
Pan troglodytes cDNA to mRNA Pan troglodytes
                                     L24922
L24922.1 GI:557728
                                                               Pan troglodytes mRNA sequence,
                                                                              CHPCR1Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prepared with primer pairs provided by Sandoz,
-- Washington University/Merck EST sequence.
Location/Qualifiers
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   Taq Polymerase:
   Total Vol;
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25. .49
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PCR Cycles:
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/db_xref="taxon:9606"
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3'end of ORF
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for 23 seconds
for 30 seconds
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          591 bp
Sequence 2 from Patent WO9839433
A86593 GI:6735168
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SCRNPEDPYNOMYHVIKDIQFGSQIKYSCTKGYRLIGSSSAFGIISGNTVINONKTPV
CDRIIGGLPFTIANGDFTSISREYFHYASVYTYHCNIGSGGKKKYFELVGEPSIYCTSK
DDVGIWSGPAPQCIIRUKCTPPNYERGILVSDURSLESLUNEVEFRCQDGFYWKGPR
HYHCQALNKWEEELPSCSRVCQPPDVLHGERTQRDKDNFSPGEEVYYSCEPGYDLRG
STYLHCTPQGDWSPEAPRCEVKSCDDFLGQLPWGRVLFPLNIQLGAKVDFVCDEGFQL
KGSSASYCVLAGMESLWNSSVPVCERKSCETPPVPNGMYHVITDIHVGSRINXSCIT
GFRLKGRSGASHCVLAGMKALWNSSVPVCEDIFCOPPPAILUGHTGFPLGDIPYGKEV
SYTCDPHPDRGWTFNLIGESTIRCTSDPHGNGVWSSPAPRCELPVGAGSHDALIVGTL
LGTIIFILIIFLY"
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/db_xref="GI:557729"
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/db_xref="taxon:9598"
/cell_line="EBV transformed"
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97.58;
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                                                                                                                        unidentified.
unidentified
unclassified.
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1 (bases 1 to 591)
2 (chi)-Like Sequences Complement Receptor Type 1 (cr1)-Like Sequences Patent: WO 9839433-A 2 11-SEP-1998;
2 SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC Location/Qualifiers
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                                                                                                                                                                                 Sequence
A86601
                                                 1 (bases 1 to 591)
1 (bases 1 to 591)
Smith,R.A. and COX,V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
PATENT: WO 9839433-A 10 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unclassified.
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/db_xref="taxon:32644"
159 c 148 g 15
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159 c 151 g 15,
                                             1. .591
                                                                                                                                                                       GI:6735175
                                                                                                                                                                                          591 bp from Patent W09839433.
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83.3%;
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Pred. No. 9.4e-68;
""matches 61;
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Query Match

42.6%;

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267

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SOURCE
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Best Local Similarity 83.3
Matches 304; Conservative
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366 aaatcatgtcgtaatcctccagatcctgtgaatggcatggcacatgtgatcaaagacatc
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                              TTTTCTATCATCTGCCTGAAAAACTCTGTCTGGACTGGTGCTAAGGACCGTTGCCGACGT
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                                                                                                                                                                                                                                               unclassified.

1 (bases 1 to 591)
Smith,R.A. and Cox,V.F.
COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
PATENT: WO 9839433-A 12 11-SEP-1998;
SMITH RICHARD ANTONY GODWIN (GB); ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                 591 bp
Sequence 12 from Patent W09839433.
                                                                                                                                                                                                                                                                                                                               unidentified
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158 c 146 g 15:
                                                                                                                                                      42.6%; Score 267.4; DB 6; 83.3%; Pred. No. 9.4e-68; tive 0; Mismatches 61;
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364 GACCG 368
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                                              tctgccacatgcatcatctcaggcaacactgtcatttgggataataaaacacctgtttgt 545
                                                                      gacag 550
                                  AGCGCTACATGCATCTCTGGTGATACTGTCATTTGGGATAATGAAACACCGATTTGT
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Search completed: October Job time: 4235 sec 9, 2002, 17:10:18

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Run on:
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Perfect score:
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_032802:*
1: /SIDS1/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/gcgdata/g
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627
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SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cggactcagaagggacttcc.....ataataaaaatcttaaccga 627
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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    AAQ11642
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AAN91477
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                                                                               Human RECAP polynu CRI protein DNA. Entire human compl Human C3b/C4b rece Human polynucleoti DNA encoding novel CRI coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                            Description
Human CRI protein
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Sequence encouring	AAQ58894	5	1104	12.7	79.4	45	
	ABL33240	24	9888	13.5	84.8	44	
CD46 construct sub	AAT17597	17	1134	13.9	87.4	43	
construct	AAT17596	17	1134	13.9	87.4	42	
wild-type	AAT17595	17	1134	•	87.4	41	
construct	AAT17598	17	1134	13.9		40	
construct	AAT17599	17	945	13.9	87.4	39	
encoding no	AAS64474	23	7821		88	38	o
CAB-2 DNA. Uniden	AAD08170	22	1848	•	88.8	37	
5	AAD20355	22	1848		88.8	36	
Human immune syste	ABL33241	24	9888	٠	103.4	ω 5	a
CD46 clone pm5.6.	AAQ14916	12	1991	•	103.4	34	
CD46 clone pmb.1.	AAQ14915	12	1659	16.5	103.4	ω ω	
CD46 clone pm5.8.	AAQ14919	12	1244	16.5	103.4	32	
Membrane co-factor	AAT46065	17	1878	18.6	116.6	31	
Sequence encoding	AAQ10864	12	1546	18.8	117.6	30	
Human CD46 cDNA.	AAT03339	16	1530	18.8	117.6	29	
Human MCP (CD46) I	AAQ99106	16	1530	18.8	117.6	28	
ng nove	AAS64470	23	1437	19.1	120	27	
DNA encoding novel	AAS64286	23	1437	19.1	120	26	
Human biallelic po	AAX11827	19	125	19.9	124.6	25	a
Human secreted pro	AAC04275	21	396	24.5	153.6	24	
Lung cancer associ	AAF18270	21	3308	24.9	156.4	23	
cance	AAH34933	22	3302	24.9	156.4	22	
Human MCP cDNA. H	AAT90306	18	1477	24.9	•	21	
Human C3b/C4b rece	AAZ38151	20	5420	34.9		20	
Partial human comp	AAQ11643	12	5420	34.9	•	19	
DNA encoding novel	AAS64289	23	2798	39.5	•	18	
Complement recepto	AAV53273	19	591	42.6	•	17	
	AAV53272	19	591	42.6	267.4	16	
	AAV53271	19	591	2	267.4	15	
	AAV53270	19	591	42.6	267.4	14	
	AAV53269	19	591	•	267.4	13	
	AAV53262	19	591		267.4	12	
₽	AAS64473	23	2796	43.0	269.4	11	
	AAS64290	23	9038	43.6	273.2	10	

ALIGNMENTS

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AAF58602
                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                             21-JUL-1999;
07-OCT-1999;
12-NOV-1999;
                                                                                                                                                                                                      Human; RECAP; receptors and associated proteins; cerebroprotective; nootropic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV; antidabetic; immunostimulant; immunomodulator; antilinflammatory; antithyroid; immunosuppressive; nephrotropic; antigout; thyrominetic; cytostatic; antibacterial; virucide; fungicide; protozoacide;
                                                                                                                                                                                                                                                                            Human RECAP polynucleotide,
                                                                                                                                                                                                                                                                                                       24-APR-2001
                                                                                                                                                                                                                                                                                                                              AAF58602;
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                                                                                            21-JUL-2000; 2000WO-US20035
                                                                                                                      01-FEB-2001.
                                                                                                                                             WO200107612-A2
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                            antiarteriosclerotic; hepatotropic; gene therapy; infection; cancer; ss
                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                              Д
                                                                                                                                                                                                                                                                                                      (first entry)
                                              99US-0145232.
99US-0158578.
99US-0165192.
Tang YT,
                                                                                                                                                                                                                                                                                 SEQ ID NO: 30.
  Yue H,
  Azimzai
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Au-Young

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Bandman O,

Υ,

Burford

Lal P;

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, dementia, Parkinson's disease, Downs's syndrome, amyotrophic lateral sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD (Creutzfeldt-Jakob disease), GSS (derstmann -Straussler-Scheinker syndrome); immunological disorders, including autoimmune/inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel receptors and associated proteins for diagnosis and treatment of neurological disorders, immunological disorders including autoimmune/inflammatory disorders and cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human RECAP (receptors and associated proteins) polypeptide. RECAP polymucleotides and polypeptides are useful in the diagnosis, treatment and prevention of neurological disorders such as stroke, Alzheimer's disease, Pick's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 120; 128pp; English
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P-PSDB; AAB68878.
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627; Conserva
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Pred. No. 5.5e-181;
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Query Match Best Local :

410;

Conservative

Similarity

56.1%;

Score 352; DB 10; Pred. No. 1.3e-96; 0; Mismatches 75;

Length 6951;

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Gaps

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RESULT
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                        This is full-length CRI protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity They are useful in diagnosing and treating immune disorders, and prevented the convertase activity.
                                                                                    New nucleic acid sequences encoding new CR1 protein - and its for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc
                                                                                                                                                                                                                                                                                                                         CDS
                                                                      Claim
                                                                                                                                                                                                         01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                       Complement;
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Sequence 6951 BP; 1802 A;
                  perfusion injury.
                                                                                                                          P-PSDB;
                                                                                                                                                   Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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THE JOHNS HOPKINS UNIVERTHE BRIGHAM AND WOMENS
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                                                                                                                                                                                                                                                                                                                                                                                      (human).
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28..1533
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28..6147
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/note="CR1 protein
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       Fearon DT,
Makrides SC,
                                     (TCEL-) T CELL SCI INC.
(UYJO) JOHNS HOPKINS UNIVERSITY
(BRIG-) BRIGHAM AND WOMEN'S HOSP:
                                                                             26-SEP-1989;
26-SEP-1990;
                                                                                                            25-SEP-1990;
                                                                                                                                18-APR-1991
                                                                                                                                                     WO9105047-A
                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                         complement system; C3b/C4b receptor; CR1; allergic reaction; immune response; clone lambda T109.1; ss.
                                                                                                                                                                                                                                                                                                       Entire human complement type 1 receptor coding region.
                                                                                                                                                                                                                                                                                                                             25-JUN-1991
                                                                                                                                                                                                                                                                                                                                                 AAQ11642;
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       Klickstein LB,
;, Marsh HC;
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                             89US-0412745.
90US-0912349.
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/note= "putative"
148..6144
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                                      HOSPITAL.
                Wong WW,
                 Carson
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RESULT
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Best Local Similarity
Matches 410; Conserv
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                                                                               AAZ38150 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      damage due to inflammmation and in treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial i
                                                 AAZ38150;
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P-PSDB; AAR11810.
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                                                                                                                                                                                         tgtgacag 550
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                                                                                                                                                                                                                                                                                                                                                ccgttttctatcatctgcctaaaaaactcagtctggacaagtgctaaggacaagtgcaaa
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                                                                                                                                                                                                                         tcgtctgccacatgcatcatctcaggtgatactgtcattttgggataatgaaacacctatt
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                                                                               DNA; 6951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.1%;
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Pred. No. 1.3e-96;
0; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6951;
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422

387

507

447

362

267

207

22-FEB-2000

(first entry)

C3b/C4b

receptor (CR1) protein encoding DNA.

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Matches
                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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06-DEC-1974;
24-FEB-1993;
01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human C3B/C4B receptor (CR1) protein. The CR1 protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full length human CR1 as expressed on erythrocytes. The CR1 function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CR1 protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CR1 protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CR1 proteins, analogues, derivatives, and anti-CR1 antibodies are used in assays, and diagnostics. The present sequence represents a DNA encoding the human CR1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-633357/54.
P-PSDB; AAY55751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 6951 BP; 1802 A; 1680 C; 1661 G; 1808 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A-P; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiant activity
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(BGHM ) BRIGHAM & WOMENS HO
(AVAN-) AVANT IMMUNOTHERAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart condition; autoimmune disorder; diagnostic; ss.
                                                                  148 ggtcaatgcaatgccccagaatggcttccatttgccaggcctaccaacctaactgatgag
                                                                                                                                                           126 cggcgctttcctgggtttctctggcggccctggtgttgct---gctgtcctccttctcc 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human C3B/C4B receptor (CR1) protein having antiinflammatory and
                                                                                                                                      66
                                                                                                                                                                                                                                                                                                  Local Similarity
tttgagtttcccattgggacatatctgaactatgaatgccgccctggttattccggaaga
                                                                                   gatcaatgcaatgtcccggaatggcttccatttgccaggcctaccaacctaactgatgac
               tttgagtttcccattgggacatatctgaactatgaatgccgccctggttattccggaaga
                                                                                                                                                                                                                                    410;
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Carson GR;
                                                                                                                                                                                                                                                                                     Conservative
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74US-0350238.
93US-0026134.
88US-0176532.
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                                                                                                                                                                                                                                                                                                    56.1%;
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                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                 Score 352; DB 20;
Pred. No. 1.3e-96;
0; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                   Length 6951;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                           Tang
Wang
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide
                                                                                                                                                                                                                                                                                                     Zhao
                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI58380 standard; cDNA; 7313 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokinetic; thrombolytic; drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia; ss.
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                                                                                                                                                                                                                                                                                                   Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC.
                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0488725.
; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0653936.
; 2000US-0639336.
; 2000US-0727344.
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                                                                                                                   NO 583;
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Wehrman T,
                                                                                                                                                                                                                                                                                                          Goodrich R,
                                                                                                                   10078pp;
                                                                                                                                                                                                                                                                                                     Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT;
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                                                                                                                   English.
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7313
 WO200175067-A2
                                                                                              DNA encoding
                                                                                                                             13-FEB-2002
                                                                                                                                                                                  AAS64474 standard; cDNA; 7821
                             Homo
                                                                                                                                                       AAS64474;
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The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                               tcgtctgccacatgcatcatctcaggtgatactgtcatttgggataatgaaacacctatt
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                                                         mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss
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730

tggacaagtgctaaggacaagtgcaaacgtaaatcatgtcgtaatcctccagatcctgtg

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ctggtgttgctgctgctccttctccgatcaatgcaatgtcccggaatggcttccattt 215 gttgggcagccggcccggtctccccttctgctgcggaggatccctgctggcggtcgtg cccqtccgtctcgagcgtccctttccttcccggcgctttcctgggttgcttctggcgcc 155

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336

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypurase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polypucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (III). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as considered in the same of the suseful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of this pattent did not appear in the printed consectification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
Query Match
Best Local Similarity
Matches 413; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000;
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                                                                                        Sequence
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DB; ABG00287.
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80.2%;
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 Score 351.8;
Pred. No. 1.6e
0; Mismatches
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                         1.6e-96
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Claim 1; Fig 1; 90pp;

English

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ID AAQ4
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Nucleic acid encoding polypeptide having complement regulatory activity - used to prevent reperfusion injury, inhibit Arthus reaction and neutrophil mediated tissue damage and reduce myocardial infarct size and inflammation
                                                                                                                          (BGHM )
(TCEL-)
(UYJO )
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                                                                                          Carson GR, (
Makrides SC,
                                                                                                                                                                        01-APR-1988;
03-APR-1989;
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DB; AAR36743.
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T CELL SCI INC.
UNIV JOHNS HOPKINS.
                                                                                          Concino MF, Wong WW;
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89US-0332865.
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/note= "CR1 |
509..512
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                                         CC molecular weight as membrane-associated CR1. CR1 binds C3b and C4b C2 that have covalently attached to immune complexes and other complement CC activators. The consequences of these interactions depends on the CT type of bearing the receptor. Erythrocyte CR1 binds immune complexes (CC type of bearing the receptor. Erythrocyte CR1 binds immune complexes (CC internalises bound complexes, either by adsorptive endocytosis is less (CC or by phagocytotsis. The function of CR1 on B lymphocytes is less (CC well defined. CR1 can inhibit the classical and alternative pathway (CC 3/C5 convertases and act as a cofactor for the cleavage of C3b and (CC 4b by factor I, therefore CR1 has a complement regulatory function (CC as well as acting as a receptor. CR1 is a glycoprotein composed of (CC as well as acting as a receptor. CR1 is a glycoprotein composed of (CC as ingle polypeptide chain. Four allotypic forms of CR1 have been (CC common forms, the F and S allotypes, also termed A and B allotypes, have molecular weights of 250 and 290 kD respectively. The two most (CC common forms, the F and S allotypes, also termed A and B allotypes, composed of common forms, the properties of approx. 40-50 kD. The two rarer (CC common forms, the F and S allotypes, also termed A and B allotypes, also termed A and B allotypes, (CC common forms, the F and S allotypes, also termed A and B allotypes, (CC common forms, the properties of 250 and 290 kD. These differences (CC common forms, the properties with endoglycosidase F. The CR1 gene has completed by treatment of the purified receptor portein with endoglycosidase F. The CR1 gene has completed by treatment of the deep subject the subject of the larger allotypes.
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6951 BP;
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1799 A; 1692 C; 1648 G; 1807 T; 5 other;

Query Match Best Local Similarity

55.5%; 83.2%;

DB 14; 2.2e-95;

Length 6951;

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                                                                                         atccagttcggatcccaaattaaatattcttgtactaaaggataccgactcattggttcc
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sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a cc nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which cc bind to polypeptides of the invention Although novel, many of the cc polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities; and hence cc potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; cativin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombotytic activities; activin- or inhibin-related activities; or may be call proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), atherometal activities (e.g., asthma or arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; tissue regeneration; wound healing; infection; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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DB; ABB11782.
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2000US-0560875.
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activin;
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atherosclerosis,

coronary heart

RRESULT
RAIGOLT
AAIGOLT
XX
AC AAIG
XX
Z2-C
DT 22-C
DT 22-C
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DE Huma
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Huma
KW Huma
KW Alzk
KW Alzk
KW Alzk
KW Angeri

22-OCT-2001

(first entry)

AAI60166 standard;

CDNA; 7028

9

Human polynucleotide SEQ ID

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

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CC vascular growth. Polypeptides involved with tissue regeneration and cC repair (or nucleic acids encoding them) may be used to promote wound CC healing (e.g., of burns, incisions and ulcers), while those with CC immunomodulatory activities may be used in the treatment of viral, CC bacterial and fungal infections in addition to immune disorders. CC Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to CC manipulate stem cells in culture to give rise to neuroepithelial cells CC that can be used to augment or replace cells damaged by illness, CC autoimmune disease or accidental damage. The polypeptides and nucleotides corrections techniques. The present sequence represents a cDNA encoding a CC novel human polypeptide of the invention.
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                                                                                                                                                                        acgtaaatcatgtcgtaatcctccagatcctgtgaatggcatggtgcatgtgatcaaagg
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Pred. No. 3e-93;
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Query Match
Best Local Similarity
Matches 410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as alzheimer's, parkinson's disease, Huntington's disease, such as Alzheimer's, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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Note: The sequence data specification.
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gtttgagtttccccattgggacatatctgaactatgaatgccgccctggttattccggaag
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DB; AAM41010.
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Zhou P,
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2000US-052317.
2000US-059B042.
2000US-0520312.
2000US-0620312.
2000US-0653450.
2000US-0663191.
2000US-0593036.
2000US-0727344.
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system injuries -
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R, Drmanac R
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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WO200175067-A2
                                                                                                    DNA encoding
                                                                                                                                  13-FEB-2002
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                                                         chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder;
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86.6%;
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Pred. No. 1.6e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC constant protection of (II) is sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC and supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC amino acid sequences. AAS64197-AB594564 represent novel human CC amino acid sequences of that and products dependent on DNA and CC amino acid sequences of the invention.

CC of the polypeptide and products dependent on DNA and CC appecification, but was obtained in electronic format directly from WIPO as the polypeptide and products of the printed of the polypeptide and products of the printed of the polypeptide and products of the polypeptide and products of the printed of the polypeptide and products of the polypeptide an
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23-AUG-2000;
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                atcaaagacatccagttcggatcccaaattaaatattcttgtcctaaagga
                                                                                                        aagtgcaaacgtaaatcatgtcgtaatcctccagatcctgtgaatggcatggcacatgtg
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                                                                                                                                                                                                                                                                                                                                                              ccatcggaaatcaatgcaatgtcccggaatgggcttccatttgccaggcctaccaaccta
                                                                                   aagtgcaaacgtaaatcatgtcgtaatcctccagatcctgtgaatggcatggcacatgtg
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2000US-0649167.
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AAV53262 standard; DNA; 591

ВP

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AAV53262
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AAV5
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      control of the complement of the SCR3 of CR1-like pseudogene (see AAW79247). CM7 DNA was constructed using plasmid pDB1013-5, which codes for SCR1-3 of CR1, by site-directed mutagenesis using 3 pairs of oligonuclectides (see AAV53263-65) that introduced 10 amino acid changes to the native SCR3 sequence corresponding to changes conserved in the CR1-like pseudogene (Cr1pse). PBRTOCSCR1-3CM7 Carrying the CM7 DNA construct was used to transform Escherichia coli BL21(DE3), and CM7 was purified from solubilised inclusion beddies. The invention provides DNA sequences (see AAV53262 and CMAV53269-79) encoding novel soluble engineered CR1 polypeptides (see CC AAV53269-79) encoding novel soluble engineered CR1 polypeptides (see CC AAW53264-7) such as CM7 that act as complement inhibitors with CC activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement activation, cs. such as neurological disorders (e.g. multiple sclerosis and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), CC immune complex disorders and mount of sepsis, including and mount of sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soluble polypeptide comprising short used to treat disorders and diseases inappropriate complement activation
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autoimmune disease; rheumatoid arthritis;
myasthenia gravis; reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement receptor tyre and in hammaltion; Crohn's disease; asthma; xenograft rejection; inflammation; Crohn's disease; asthma; xenograft rejection; inflammation; infection; sepsis
      Sequence
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anti-haemolytic; multiple sclerosis; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the short consensus repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence encodes CM7 (see AAW79236), a protein that conhe short consensus repeats (SCR) 1 and 2 from the complement type 1 (CR1) fused to the SCR3 of CR1-like pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-506358/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADPROTECH PLC
      591
                                                                                                     proliferative nephritis and myasthenia
      BP;
                                                                         disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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      132 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type 1-like sequence CM7 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEI,
   159 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith RAG;
      148 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      consensus repeats from LHR-A associated with inflammation
      152
      H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative nephritis;
0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein that consists
                                                                                                 gravis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sepsis;
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Ş

186

caatgcaatgtcccggaatggcttccatttgccaggcctaccaacctaactgatgacttt 245

Query Match Best Local Matches

Local was 304;

Similarity

42.6%; 83.3%;

Score 267.4; Pred. No. 2.

.5e-71

DВ

19;

Conservative

0;

Mismatches

61;

Indels Length

0;

Gaps

0

This DNA sequence encodes CM1 (see AAW79237), a protein that consists of the short consensus repeats (SCR) 1 and 2 from complement receptor type 1 (CR1) fused to an SCR3 (see AAW79242) in which 5 amino acids were altered to those found in the SCR3 of the CR1-like

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AAV53269
IID AAV5
XX
AC AAV5
AC AAV5
XX I8-J
XX Comp
XX Comp
KW Comp
KW Aenci
KW Aenci
KW Pan
KW WO9E
XX WO9E
XX WO9E
XX Pan
KW 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩV
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                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement receptor type-1; CR1; CM1; complement; inhibitor anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis autoimmune disease; rheumatoid arthritis; proliferative nep
                                                                                                                                                                                                               Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation
                                                                                                                                                                                                                                                                                                                                                                                     Cox VF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV53269 standard;
                                                                                                                                                                                      inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADPR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546
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DB; AAW79237.
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                                                                                                                                      Page 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor type 1-like sequence CM1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                         complement activation
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                                                                                                                                 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor;
                                                                                                                                                                                                                     or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   545
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Best Local Similarity
                      Complement receptor type-1; CR1; CM2; complement; inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative nephritis; myasthenia gravis; reproductive disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or disorder associated with inflammation or inappropriate complement activation, such as neurological disorders (e.g. multiple sclerosis and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory disorders (e.g. Crohn's disease, asthma, and acute pancreatitis), post-isohaemic reperfusion conditions, infection or sepsis, arthritis, proliferative nephritis and myasthenia gravis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudogene (Cripse) putative product. CMI DNA was constructed by site-directed mutagenesis (see AAV53263) of plasmid pDB1013-5, which codes for SCR1-3 of CR1. pBrocSSCR1-3CM1 carrying CM1 DNA was used to transform Escherichia coli BL21(DB3), and CM1 was purified from solubilised inclusion bodies. The invention provides DNA sequences (see AAV53262 and AAV53269-79) encoding novel soluble engineered CR1 polypeptides (see AAV53236-47) such as CM1 that act as complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 591 BP; 127 A; 159
                                                                                                                                                         Complement
                                                                                                                                                                                         18-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                     AAV53270 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reproductive disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cagttcggttcccaaattaaatattcttgtactaaaggttaccgtctgattggttcctcc
                                                                                                                                                         receptor type 1-like sequence CM2 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC of the short consensus repeats (SCR) 1 and 2 from complement within the SCR3 of the CRI-11ke pseudogene (Cripse) putative product. CM2 DNA was constructed by CC site-directed mutagenesis (see AAV53264) of plasmid pDB1013-5, which codes for SCR1-3 of CRI. pBrocSCR1-30M2 carrying CM2 DNA was used to transform Escherichia coll BL21(DE3), and CM2 was purified from CC solubilised inclusion bodies. The invention provides DNA sequences (see AAV53262 and AAV53269-79) encoding novel soluble engineered CR1 polypeptides (see AAW53364-47) such as CM2 that act as complement inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or CC disorder associated with inflammation or inappropriate complement activation, such as neurological disorders (e.g. multiple sclerosis and Parkinson's disease), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection), inflammatory CC disorders (e.g. Crohn's disease, asthma, and acute pencreatitis), CC post-ischaemic reperfusion conditions, infection or sepsis, cCC immune complex disorders and autoimmune diseases (e.g. rheumatoid CC archivetive disorders and autoimmune diseases (e.g. rheumatoid CC reproductive disorders.
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P-PSDB; AAW79238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 45; 67pp; English.
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                                                                      aaatcatgtcgtaatcctccagatcctgtgaatggcatggcacatgtgatcaaagacatc
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RESULT 15
AAV53271
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AC AAV532
DT 18-JAN
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DE Comple
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CC This DNA sequence encodes CM2 (see AAW79239), a protein that consists CC of the short consensus repeats (SCR) 1 and 2 from complement CC receptor type 1 (CRI) fused to an SCR3 (see AAW79244) in which 1 amino CC acid was altered to that found in the SCR3 of the CRI-like CRI pseudogene (Crlpse) putative product. CM3 DNA was constructed by CC site-directed mutagenesis (see AAV53265) of plasmid pDB1013-5, which Cc codes for SCR1-3 of CRI pBrocSCR1-3CM3 carrying CM3 DNA was used CC to transform Escherichia coll BL21(DE3), and CM3 was purified from CC solubilised inclusion bodies. The invention provides DNA sequences (see AAV53262 and AAV53269-79) encoding novel soluble engineered CRI CC inhibitors with functional complement inhibitory, including anti-haemolytic, activity. These can be used to treat a disease or CC disorder associated with inflammation or inappropriate complement CC anti-haemolytic, activity. These can be used to treat a disease or CC disorder associated with inflammation or inappropriate complement CC complement activation (e.g. xenograft rejection), inflammatory CC disorders (e.g. Crohn's disease, disorders of inappropriate or undesirable CC complement activation (e.g. xenograft rejection) inflammatory CC complement disorders (e.g. crohn's disease, asthma, and acute pancreatitis), CC post-ischaemic reperfusion conditions, infection or sepsis, rheumatoid CC architits, proliferative nephritis and myasthenia gravis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement receptor type-1; CR1; CM3; complement; inhibitor; anti-haemolytic; multiple sclerosis; Parkinson's disease; xenograft rejection; inflammation; Crohn's disease; asthma; pancreatitis; post-ischaemic reperfusion; infection; sepsis; autoimmune disease; rheumatoid arthritis; proliferative neph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble polypeptide comprising short consensus repeats from LHR-A used to treat disorders and diseases associated with inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 46; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cox VF,
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Search completed: October Job time: 3772 sec 9 2002,

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Listing first 45 summaries
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    393.6
352
344.8
326.8
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270.4
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5308.096 Million cell updates/sec
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A1240881 qJ94e04.x
A1718588 as446n1.x
BM477528 AGENCOURT
A173549 at11h03.x
H73873 ys14d08.r3
T66824 ya50b08.r3
T66823 ya50b08.r3
T66824 ya50b08.r3
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465 bp mRNA linear EST 10-AUG-2000 hw29d02.xl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:3184323 3' similar to 9b:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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Location/Qualifiers
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Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy
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/clone="TMAGE:318433"
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: kidney; Vector:
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Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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601905704F1 NIH_MGC_54 Homo s
mRNA sequence.
                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
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CACCTGT
                            tgtttgt 545
                                                                           ttcctcgtctgccacatgcatcatctcaggcaacactgtcatttgggataataaaacacc
                                                                                                                                                                                       AACGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATGGCACCATGTGATCAAA
                                                                                                                                                                                                                                                                     gaccgttttctatcatctgcctaaaaaactcagtctggacaagtgctaaggacaagtgca
                                                                                                                                                                                                                                                                                                                                       actttgagtttcccattgggacatatctgaactatgaatgccgccctggttattccggaa
                                                                                                                                                                                                                                                                                                                                                                                    CCGATCAATGCAATGTCCCGGAATGGCTTCCATTTGCCAGGCTACCAAACCTAACTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaatcacggggtctcccgcgcccctttc 120
                                                            TTCCTCGTCTG.
                                                                                                                                                                                                                                                      GACCGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACAAGTGCTAAGGACAAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGACTCAGAAGGGACTTCCCTGCTCGG-TGGCTTTCGGTTTCTCTGCTCACCTCCGGAT
                                                                                                                                                                                                                                                                                                                      ACTTTGAGTTTCCCCATTNGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone="Inwar: %1.3.2.2"
/Clone=lib="NIH MGC.54"
/Clone_lib="NIH MGC.54"
//tissue_type="from chronic myelogenous leukemia"
//lab_host="DH1DB (T1 phage resistant)"
//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfi! (ggccgctcggcc); Site_2: Sfi! (ggccattatggcc);
Site_1: Sfi! (ggccgctcggcc); Site_2: Sfi! (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCARTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGTGGCCCAATG-dT(30)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
188 a 226 c 197 g 220 t 1 others
571
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/db_xref="taxon:9606"
/clone="IMAGE:4133424"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 443.6; DB 10;
Pred. No. 2.9e-112;
0; Mismatches 20;
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                                                                                                                                                                                    365
                                                                                                                                                                                                                                                                                                                                                                                                                 443 TCAATGCAATGTCCGGAATGGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGACTC 384
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gtctgccacatgcatcatctcaggcaacactgtcatttgggataataaaacacctgtttg
                                                                                                                                                              taaatcatgtcgtaatcctccagatcctgtgaatggcatggcacatgtgatcaaagacat 424
                                                                                                                                                                                                                                                      gttttctatcatctgcctaaaaaactcagtctggacaagtgctaaggacaagtgcaaacg
                                           CCAGTTCGGATCCCAAATTAAATATTCTTGTCCTAAAGGATACCGACTCATTGGTTCCTC
                                                                      ccagttcggatcccaaattaaatattcttgtcctaaaggataccgactcattggttcctc
                                                                                                                                        TAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATGGCACATGTGATCAAAGACAT
                                                                                                                                                                                                                             GTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACAAGTGCTAAGGACAAGTGCAAACG
                                                                                                                                                                                                                                                                                                                     TGAGTTTCCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438;
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similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)
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AI240881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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Insert Length: 625 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1867134"
/clone_lib="NCI_CGAP_Kid3"
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Pred. No. 5.6e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoeimage.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White, Y., Wylie, T., Waterstt
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Mart,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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444 bp mRNA linear EST 10-JUN-1999
as46h01.xl Barstead aorta HPLRB6 Homo sapiens CDNA clone
IMAGE:2320273 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                134
                                                                                                                            the modified pT7T3 vector. Library constructed by Bob
Barstead."
87 c 103 g 120 t
                                                                                                                                                                                                                                                     3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTCGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2320273"
                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Barstead aorta HPLRB6"
                                                                                                                                                                                                                                                                                                                                                             'dev_stage="adult, age 64"
                      62.8%;
Score 393.6; DB 9;
Pred. No. 1.7e-98;
0; Mismatches 24;
                                          Length 444;
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AGENCOURT_6484929 NIH_MGC_85
5', mRNA sequence.
BM477528
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1 (bases 1 to 1063)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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EST.
                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 749.
                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                 251
                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9666"
/clone="IMAGE:5554371"
/clone_1lb="NNH_MGC_85"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
So thers
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  56.1%;
84.0%;
  Score 352; DB 10;
Pred. No. 8.3e-87;
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Homo sapiens cDNA clone IMAGE:5554371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcgctttcctgggttcttggcgccctggtgtttgct---gctgtcctccttctcc 182
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                                                                                                                                                                                                                         White,Y., Wylie,T., WashU-NCI human EST I
WashU-NCI human EST I
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410;
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356 bp mRNA linear EST 14-JUN-1999
atllh03.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
atllh03.x3 Similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                         Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                             Hillier,L., Allen,M., Bowles,L.,
Krizman,D., Kucaba,T., Lacy,M., J
                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 356)
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                  IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco.
                                                                                                                     This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                         rizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin I., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., itte,Y., Wylie,T., Waterston,R. and Wilson,R.
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                                                                                                                                      est@watson.wustl.edu
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/clone="IMAGE:2354837"
              /organism="Homo sapiens"
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                                                                 Location/Qualifiers
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Matches 349; Conserv
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                                                                                                                                                                                                                                                                                                                                                           H73873
440 bp mRNA linear EST 31-OCT-1995
ys14d08.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:214767 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
1_PRECURSOR (HUMAN);, mRNA sequence.
                                                             Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 5 (9), 807-828 (1996)
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 440)
                                                                                                                                                                                                                                                                                                                           H73873.1 GI:1046874
                                                                                                                                                                                                                                                                          Homo sapiens
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                  Contact: Wilson RK
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a 61 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the modified pT7T3 vector. Library constructed by Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested with Not I and cloned into the Not I and Eco RI sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Barstead
/sex="male"
/dev_stage="adult, ag
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98.0%;
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                                                                                                                                         ttgagtttcccattgggacatatctgaactatgaatgccgccct-ggttattccggaaga
                                                                                                                                                                                                                                                                                                                     tcacqqqgtctcccgcgccgctcatggcgcctcccgtccgtctcgagcgtccctttcctt 123
                                                                                                                                                                                    ACGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 706 Std Error: 0.00 Seq primer: M13RP1
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Source: IMAGE Consortium,
                           T66824

346 bp mRNA linear EST 07-MAR-1995
ya50b08.r3 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:66327 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1
          T66824
                    PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
 GI:676264
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98.4%;
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                                                                                                                                                                                                     132
                                                                                                                                                                         Match 49.0%; Local Similarity 98.3%;
                                                                                                                                                                                                                      1 TOTOCCGCGCCCCTCATGGC-CNTCCCGTCCGTCTCGAGCGTCCCTTTCCTTCCCGGCGC 59
                                catgtcgtaatcctccagatcctgtgaatggcatgggcacatgtgat 415
                                                                                           cccattgggacatatctgaactatgaatgccgccct-ggttattccgggaagaccgttttc 310
                                                                                CCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGGTTATTCCGGAAGACCGTTTTC
                                                                                                                                                                                       340;
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The Washb-Merck EST Project
Unpublished (1995)
Other_ESTs: ya50b08.s3.exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stops: 324
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Bark Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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314 286 1810
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="TMAGE:66327"
/clone_lib="Soares fetal liver spleen lNFLS"
/cse="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Primates;
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322 taaaaaactcagtctggacaagtgctaaggacaagtgcaaacgtaaatcatgtcgtaatc
                                                                                                                                                                                                                                                               Local Similarity
TAAAAAACTCAGTCTGGACAAGTGCTAAGGACAAGTGCAAACGTAAATCATGTCGTAANC
                                                                                                                                                         CTGAACTATGAATGCCCGCCCCTGGTTANTCCCGGAAGACCGTTTTCCTATCATCTGCCC
                                                                                                                                                                               ctgaactatgaatgc---cgccctggttattccggaagaccgtttt-ctatcatctg-cc 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Source: IMAGE Consortium, LINL
This clone is available royalty free through LINL;
IMAGE Consortium (info@image.llnl.gov) for further:
Seq primer: -21Mi3LR
High quality sequence stop: 390.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="IMAGE:66327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares fetal liver spleen lNFLS"
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   336;
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1 (bases 1 to 541)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,J., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T83269 541 bp mRNA linear EST 16-MAR-1995 yd41a11.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110780 5' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 791
High quality sequence stops: 300 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 791 Std Error: 0.00
Seq_primer: M13RP1
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                 Similarity
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314 286 1810
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   Conservative
                                                                                /db_xref="taxon:9606"
/clone="IMAGE:110780"
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                 /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                 43.1%;
93.9%;
   0;
                 Score 270.4; DB 1
Pred. No. 2.9e-64;
   Mismatches
                              DB 10;
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                              Length
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WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 433)
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                                                                                                                                                                                                                                         High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                      /sex="male"
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ATCATCTGCCTAAAAAACTCAGTCTGGACAAGTGCTAAGGACAAGTGCAAACGTNAAATC
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433 bp mRNA linear EST 14-JUN-1999
as44f09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2320073 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE
                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR (HUMAN);, mRNA sequence.
                     the modified pT7T3 vector. Library constructed by Bob
                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2320073"
/clone_lib="Barstead aorta HPLRB6"
                                                                                                                                 /dev_stage="adult, age 64"
/lab_host="DH10B (phage re
                                                                                                                                                                                                                                                                           60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc-aaattaaatattettgteetaaaggataeegaeteattggtteetegtetgeeaeat 495
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                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3013 row: A column: 12
Seg primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 577) (bases 1 to 577) (Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
                                                                                                                                                                                                                                   Contact: George J. Kargul Laboratory of Genetics
                                                                                                                                                                                                                                                                       Verification and initial Unpublished (2001) Other_ESTs: H3013A12-3
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                                                                        POLYA=No
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             1. .577
/organism="Mus musculus"
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Pred. No. 8.4e-64;
0; Mismatches 74
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NA Clone
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Best Local Similarity 71.48;
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                                                                                                                                                                                                                                                                                                                                TGGACGAGTGCTGAAGATAAGTGTATACGAAAACAATGTAAAACTCCTTCAGATCCTGAG
mp08b07.rl Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA clone TMAGE:588597 5' similar to gb:M23529 Mus musculus complement receptor (MOUSE);, mRNA sequence.

AA107525 GI:1659424
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Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: psporm1; Site_1: Salı; Site_2: Not1; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of £7.5 embryos, extraembryonic part of £7.5 embryos, extraembryonic part of £7.5 embryos, and £12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with oligo(drover)
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/db_xref="niaEST:H3013A12-5"
/db_xref="riaxon:10090"
/clone="H3013A12"
/clone="H3013A12"
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/dev_stage="Clones arrayed from a variety of cDNA
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Pred. No. 2.9e-48;
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GTTGATTGGGATACTGAGGCACCTATTTGTGA
              gtcatttgggataataaaaacacctgtttgtga
                                                         AATCAAGGATACCGCCTCATTGGTTCCTCCTCTGCTGTATGTCATCACTGATCAAAGT
                                                                         cctaaaggataccgactcattggttcctcgtctgccaccatgcatcatctcaggcaacact
                                                                                                                                 aatggcatggcacatgtgatcaaagacatccagttcggatcccaaattaaatattcttgt 455
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                                                                                                                                                                                                                                                                                               GCCAAACCTATAAATCTAACTGATGAATCCATGTTTCCCCATTGGAACATATTTGTTGTAT
                                                                                                                    The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 614)

1 (bases 1 to 614)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:343245
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4444 Forest Park Parkway, Box 8501, St. Ld
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Location/Qualifiers
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314 286 1810
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141 c 141 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Life Tech mouse
/tissue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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/strain="C57BL/6J"
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cctaaaggataccgactcattggttcctcgtctgccacatgcatcatctcaggcaacact
                                                                                            aatggcatggcacatgtgatcaaagacatccagttcggatcccaaattaaatattcttgt 455
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 658)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11946 row: a column: 10
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/db_xref="taxon:10990"
/clone="IMAGE:5371665"
/clone=lib="NGI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/dev_stage="5 months"
/dev_stage="5 months"
/lab_host="DHIOB"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/note="Organ: midirectionally. Primer: Oligo dT.
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
63 a 146 c 158 g 191 t
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s musculus cDNA clone IMAGE:5371665
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                                                                      GAATGTCTCCCAGGATATATCAAGAGGCAGTTCTCTATCACCTGCAAACAAGACTCAACC
                                                                                              GCCAAACCTATAAATCTAACTGATGAATCCATGTTTCCCCATTGGAACATATTTGTTGTAT
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plate: LLAM11634 row: 1 column: 18
High quality sequence stop: 795.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Copyright (c) 1993 - 2000
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US-08-482-148-8
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S514787-1
US-08-482-149-17
US-08-528-057-43
US-08-528-057-1
US-08-483-149-17
US-08-528-057-1
US-08-528-057-1
US-08-6483-149-17
US-08-6483-149-17
US-08-6483-149-11
US-08-11-11
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Patent No. 5472939
Sequence 33, Appl
Patent No. 5256642
Patent No. 5472939
Patent No. 5514787
Sequence 17, Appl
Sequence 43, Appl
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 11, Appl1
Sequence 11, Appl
Sequence 11, Appl
Sequence 31, Appl
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 2, Appl1
Sequence 2, Appl1
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8.7	8.7	8.7	8.9	9.3	9.3	9.4	9.4	9.7	12.0	12.0	12.0	12.0	13.0	13.0	13.1	13.1	13.9
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12,		Sequence 19,	Sequence 14, Appl	Sequence 7, A	Sequence 7, A	Sequence 2, Ap	Sequence 2, Ap	-	Sequence 4, Ap	Sequence 3, Ap	Sequence 4, Ap	Sequence 3, Ap	Sequence 6, Appli			Sequence 5, Ap	Sequence 4, Ap

ALIGNMENTS

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APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:1:
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5256642-1
5256642-1
;Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG, WINNE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN ;H.;MAKKIDES, SAVVAS;MARSH, HENRY C. JR.
;H.;MAKKIDES, SAVVAS;MARSH, HENRY C. JR.
;H.;TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR 1 (CR1) AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.1%;
Best Local Similarity 84.0%;
Matches 410; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 6951
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Pred. No. 3e-103;
0; Mismatches 75; Indels
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APPLICANT: FEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG, INNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN INTERPRETATION: MAKRIDES, SAVVAS;MARSH, HENRY C. JR.

TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
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Best Local Similarity
Matches 410; Conserv
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
ETLING DATE: 01-APR-1988
ETLING DATE: 01-APR-1988
ETLING DATE: 01-APR-1988
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Pred. No. 3e-103;
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US-08-769-967A-33
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Best Local Similarity
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TELEFAX: (610) 270-509
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,569
ETIING DATE: 15-May-1995
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P30423C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT: Smith, Richard A.G.
APPLICANT: Dodd, Ian
APPLICANT: Freeman, Anne Mary
TITLE OF INVENTION: Soluble CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,967A
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (610) 270-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
127
               306 ttttctatcatctgcctaaaaaactcagtctggacaagtgctaaggacaagtgcaaacgt 365
                                                                               246 gagtttcccattgggacatatctgaactatgaatgccgccctggttattccggaagaccg 305
                                                                                                                                                 186 caatgcaatgtcccggaatggcttccatttgccaggcctaccaacctaactgatgacttt 245
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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83.3%;
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Pred. No. 1.4e-76;
0; Mismatches 61
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TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR
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Best Local S
Matches 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
20 ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPTOR 1 (CR1) AND A THROMBOLTIC AGENT,
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                                                         2974
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US-08-057-45
IS-08-057-45
; Sequence 45, Application US/08528057
; Patent No. 5846715
; GENERAL INFORMATION:
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5472939-3
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TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIATED DISORDERS
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Best Local Sim
Matches 275;
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FILING DATE: 19-OCT1-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
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 3034
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0; Mismatches 94
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APPLICANT: PURCELL, Damian F. J. APPLICANT: RUSSELL, Sarah M. APPLICANT: MCKENZIE, Ian F. C. TITLE OF INVENTION: CD46 VARIANTS NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

Foley & Lardner

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-528-057-45
                                                             US-08-528-057-41
                                                                             RESULT
              Sequence 41, Application US/08528057 Patent No. 5846715 GENERAL INFORMATION:
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Best Local Similarity
Matches 172; Conserva
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APPLICATION UNMBER: US 07/961,686
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU91/00199
FILING DATE: 10-MAY-1991
PRIOR APPLICATION UNMBER: AU PK0133/90
FILING DATE: 11-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS:
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                      189 CGATGCCTGTGAGGAGCC 206
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LOCATION:
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PURCELL,
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Damian F. J
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Pred. No. 1.3e-40;
0; Mismatches 26;
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; LOCATION:
US-08-528-057-41
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Best Local Similarity
Matches 163; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 10-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PKO
FILING DATE: 11-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/yo1,000 FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR NUMBER: US 07/961,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RUSSELL, Sarah M.
APPLICANT: MCKENZIE, Ian F. C.
TITLE OF INVENTION: CD46 VARIANTS
 188 GAGGAGCC
                               192 aatgtccc 199
                                                                           NAME/KEY:
LOCATION:
                                                                                                                             68
                                                                                                                                                                                                          12 gggacttccctgctcggcttggctttcggtttctctgctcacctccggataaatcacgggg 71
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                                                                                                                                                                                         GGGACTTCCCTGCTCGGCTCTCGGTTTCTCTGCTTTCCTCCGGAGAAATAACAGCG 67
                                                            TITCCTGGGTTGCTTCTGGCGGCCATGGTGTTGCTGCTGTACTCCTTCTCCGATGCCTGT 187
                                                                                                                          20007-5109
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                                                                                                                                                                                                                                                           Conservative
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83..1192
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185..1192
195
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                                                                                                                                                                                                                                                       Score 148; DB 2; I
Pred. No. 6.4e-38;
0; Mismatches 25;
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Sequence 3, Application US/08458084 Patent No. 5624837
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Patent No. 6218520
                                                                                                                                                                                                                                                                                                                     Matches 134;
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human t-Cell Line HSB2 - 08-139-195-1
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APPLICANT: Atkinson, John P.
TITLE OF INVENTION: RECOMBINANTLY PRODUCED HUMAN MEMBRANE
TITLE OF INVENTION: COFACTOR PROTEIN (MCP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (404)-815-655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/
FILING DATE: 21-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-JUL-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                        164 gctgctgtcctccttctccgatcaatgccaatgtcccggaa 203
                                                                                                                                                                                              104 tetegagegtecettteetteeeggegettteettggttgttettggeggecetggtgtt 163
                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 20-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                TCTGCTTTCCTCCGGAGAAATAACAGCGTCTTCCGCGCCGCCGCATGGAGCCTCCCGGCCG
                                                                                                         GCTGCTGTACTCCTTCTCCGATGCCTGTGAGGAGCCACAA 160
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(404)-815-6555
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Pred. No. 2.5e-28;
0; Mismatches 26;
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; VOLUME: 168
; PAGES: 181-194
; DATE: 1988
US-08-458-084-3
                                                                Matches
                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
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DESCRIPTION:
HYPOTHETICAL: N
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CURRENT APPLICATION DATA:
APPLICATION NOTICE
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APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Chimeric Complement
TITLE OF INVENTION: Inhibitor Proteins
NUMBER OF SEQUENCES: 19
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NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,
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AUTHORS: Lublin, D.M.
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                 44 tctgctcacctccggataaatcacggggtctcccggcgccgctcatggcgcctcccgtccg 103
                                                              Local Similarity nes 132; Conserv
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CITY: Fairfield
                                                                                                                                                                                                                                                            TITLE:
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1 TCTGCTTTCCTCCGGAGAAATAACAGCGTCTTCCGCGCCGCGATGGAGCCTCCCGGCCG 60
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                                                                                                                                                                                                                                       : Atkinson, J.P.
Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for Inclusion
in the Multi-Gene Family of
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                                                                Conservative
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Arce, M.A.
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                                                                                                                                                                                                         Journal of Experimental Medicine
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MCP (CD46) full length cDNA
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                                                                              18.8%;
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                                                              Score 117.6; DB 1;
Pred. No. 4.5e-28;
0; Mismatches 24;
                                                                Indels
                                                                                            Length 1530;
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104 tetegagegtecettteetteeeggegettteetgggttgettetggeggeeetggtgtt 163

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                                                                                                                                                                                                                                                                   ORGANISM: HOMO SMF-.
ORGANISM: HOMO SMF-.
PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
AUTHORS: Liszewski,M.K.
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TELEFAX: (203) 254-1101
INFORMATION FOR EEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
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NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: AL
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
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APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Chimeric Complement
TITLE OF INVENTION: Inhibitor Proteins
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MCP (CD46) full length cDNA
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                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Dell 486/50
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
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                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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                                                                                         : Atkinson, J.P.
Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for Inclusion
in the Multi-Gene Family of
                                                                        Complement-Regulatory Proteins.
                        181-194
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1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1530 bases
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Arce, M.A.
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Rebentisch, M.B.
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Dell 486/50
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                                                       of Experimental Medicine
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TELEFAX: (203) 772 3655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1530 base paint
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/482
FILING DATE: 6/07/95
CLASSIETICATION: 530
CATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
                                                             PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
AUTHORS: Lispannin.
                                                                                                                                                                                      MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows 95 under MS DOS SOFTWARE: Microsoft Word for Windows CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible (Pentium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Terminal Complement
TITLE OF INVENTION: Inhibitor Fusion Genes and Proteins
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rother, Russell
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Terminal Complement
                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                          ORIGINAL SOURCE:
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                                                                                                                                                                                                                              TOPOLOGY: Linear
                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                    AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Seth A. Fidel
Alexion Pharmaceuticals, 25 Science Park
                                   Post, T.W.
Arce, M.A.
Rebentisch, M.B.
                                                                                                                                                          No
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                  LeBeau, M.M.
                                                                                                                                                                             No
                                                                                                                                                                                          cDNA to mRNA
MCP (CD46) full length cDNA
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Pred. No. 4.5e-28;
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STRANDEDNESS: Double

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Best Local Similarity
Matches 132; Conserv
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
           TELEFAX: (203) 254 110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
FILING DATE: 3-MAR-1994
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb storage
COMPUTER: Dell 486/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rother, Russell
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Terminal Complement
                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS 6.2
SOFTWARE: WOLD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Terminal Complement
TITLE OF INVENTION: Inhibitor Fusion Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 06430
                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                          Fairfield
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                                                                                                                                                                                                                                                                                                                                                                                                           Connecticut
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                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Maurice M. Klee
1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                            USA
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7: 8:
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Pred. No. 4.5e-28;
0; Mismatches 24
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PCT-US95-02945-3
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Best Local Similarity
SOFTWARE: WOrdPerfect 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch,
COMPUTER: Dell 486/50
                                                                                                                                                                                                                                              APPLICANT: Fodor, William L
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P
TITLE OF INVENTION: Chimeric Complement
TITLE OF INVENTION: Inhibitor Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: MCP (CD46) full length cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                    STREET: 1951 Bus
CITY: Fairfield
                                                                                                                                                                        ADDRESSEE: Mau....
smbret: 1951 Burr Street
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                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 181-194
DATE: 1988
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                                                                                                                                                          Connecticut
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Molecular cloning and Chromosomal Localization of Membrane Cofactor Protein (MCP): Evidence for Inclusion in the Multi-Gene Family
                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post, T.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lublin, D.M
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             PCT/US95/02945
                                                                                            750 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117.6; DB 5
Pred. No. 4.5e-28;
0; Mismatches 24
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ATTORNEY/AGENT

INFORMATION: 3-MAR-1994

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

PRIOR APPLICATION DATA:

08/205,508

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RESULT 14
5514787-1
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; DATE: 1988
PCT-US95-02945-3
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                                                       Patent No. 5514787

; APPLICANT: ATKINSON, JOHN P.

; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN MEMBRANE; COFACTOR PROTEIN (MCP)
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.8%;
Best Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                        Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (203) 254-1101 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
AUTHORS: Liszewski,M.K.
AUTHORS: Post, T.W.
AUTHORS: AICE, M.A.
AUTHORS: LeBeau, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-120PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-1400
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/948,350
FILING DATE: 21-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MCP (CD46) full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                            44 tetgeteaceteeggataaateaeggggteteeeggegeegeteatggegeeteeegg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: Inclusion in the Multi-Gene Family TITLE: of Complement-Regulatory Proteins. JOURNAL: Journal of Experimental Medicine VOLUME: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
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EDNESS: Double
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Molecular cloning and Chromosomal
Localization of Membrane Cofactor
Protein (MCP): Evidence for
Inclusion in the Multi-Gene Family
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Lemons, R.S.
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                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Score 117.6; DB 5; Pred. No. 4.5e-28;
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; APPLICATION NUMBER: 384,210; FILING DATE: 21-JUL-1989; SEQ ID NO:1:
                                                                                         ; TOPOLOGY: 11; MOLECULE TYPE: US-08-435-149-17
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US-08-435-149-17
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                                                                                                                                                                                                           REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0989.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
TELEFAX: N/A
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Appli
Patent No. 5866402
Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.8%;
Best Local Similarity 84.6%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
NAME: SAVEREIDE, PAUL B.
OO
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
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ADDRESSEE: CHIRON C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INNIS, MICHAEL A.
APPLICANT: ZAROR, ISABEL
APPLICANT: CREASEY, ABLA A.
TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 gctgctgtactccttctccgatgcctgtgaggagcc 156
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FILING DATE: 05-MAY-1995
CLASSIFICATION: 530
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                 18.6%;
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Pred. No. 4.5e-28;
0; Mismatches 24
Score 116.6; DB Pred. No. 1.1e-27 0; Mismatches 2
                                DB 2;
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                                  Length 1878;
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